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Express Mail Label No.: EL928105062US

Date of Deposit: July 14, 2004

Atty. Docket No.: 8822/2022

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Bachmann, et al.
Serial No.: 10/762,107
Filed: January 21, 2004
Entitled: Farnesyl Dibenzodiazepinone,
Processes for Its Production and its Use
as a Pharmaceutical

Examiner: Not yet assigned

Group Art Unit: 1624

Conf. No.: 4987

Mail Stop Missing Parts
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

PETITION UNDER 37 C.F.R. §1.182

Applicants hereby petition under 37 C.F.R. §1.182 that the above-noted application be recognized as complete as of its filing date of January 21, 2004.

In the Notice to File Missing Parts mailed May 14, 2004 it was stated that Figure 20, referred to in the specification, was **omitted** among the materials filed on January 21, 2004.

Applicants submit that Figure 20 was in fact submitted with the application. Figure 20 is the Nucleic Acid Sequence Listing, provided in both paper and computer-readable form as noted in the Transmittal Letter that accompanied the file. Copies of the following are submitted herewith in proof of timely deposit of Figure 20:

A) the Transmittal Letter, showing entry (3) as “(3) One Hundred and Fourty (sic) Seven (147) sheets of Informal Drawings of Figs 1-20, *including Figure 20 as the Paper Copy of the Sequence Listing*” (emphasis added);

B) the paper copy of the Sequence Listing itself; and

C) the date-stamped return postcard acknowledging receipt of the “Paper copy of Sequence Listing (as figure 20).”

Applicants submit that the evidence provided herein is sufficient to establish that Figure 20 was timely submitted upon filing of the application. The Commissioner is authorized to

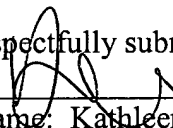
Serial No.: 10/762,107

charge the applicable \$130.00 petition fee under 37 C.F.R. 1.17(h), and any other necessary fees to Deposit Account No. 16-0085, Reference 8822/2022.

Applicants respectfully request acknowledgment that the application was complete as of the January 21, 2004 filing date.

Date: July 14, 2004

Respectfully submitted,


Name: Kathleen Williams

Registration No.: 34,380

Customer No.: 29933

Palmer & Dodge LLP

111 Huntington Avenue

Boston, MA 02199-7613

Tel: 617-239-0100



Atty. Docket No.: 8822/2022

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Bachmann, et al.
Serial No.: Not yet assigned
Filed: January 21, 2004
Entitled: Farnesyl Dibenzodiazepinone, Processes for
Its Production and its Use as a
Pharmaceutical

COPY

CERTIFICATE OF MAILING UNDER 37 CFR 1.10

I hereby certify that the paper (and any paper or fee referred to as being enclosed) is being deposited with the United States Postal Service using Express Mail to Addressee Service, under 37 C.F.R. Section 1.10, **Express** Mail Label No. EL932932039US on this date, **January 21, 2004**, postage prepaid, in an envelope addressed to Mail Stop Patent Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Mary Wilson

Name of Person Mailing Paper

Signature of Person Mailing Paper

Mail Stop Patent Application
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

TRANSMITTAL LETTER

Enclosed for filing in the above-identified patent application, please find the following documents:

1. New Patent Application Transmittal;
2. Patent Application, (142 pages);
3. One Hundred and Fourty Seven (147) sheets of Informal Drawings of Figs 1-20, including Figure 20 as the Paper Copy of the Sequence Listing;
4. Computer Readable Copy of the Sequence Listing;
5. Statement Under 37 C.F.R. §1.821(f) and (g);
6. Application Data Sheet;
7. Preliminary Amendment; and
8. Return Post Card.

Pursuant to 37 C.F.R. § 1.27, Applicant claims small entity status.

The Commissioner for Patents is hereby authorized to charge all fees to Deposit Account No. 16-0085, Reference 8822/2022. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Date: January 21, 2004



Name: Barbara Gyure

Registration No.: 34,614

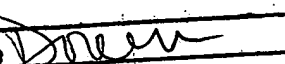
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Palmer & Dodge LLP

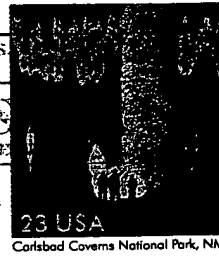
111 Huntington Avenue

Boston, MA 02199-7613

Tel: 617-239-0100

Docketed
Response Due 
Statutory Period
Palmer & Dodge LLP
Patent Department

PATENT



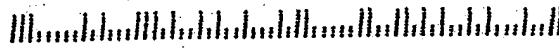
22151 U.S. PTO
10/762107



012004

Attn: Kathleen Williams
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613

012004
08/25/2004



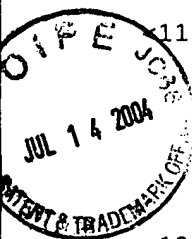
Serial No. Not yet assigned File No. 8822/2002 By: Kmw (m65)
Applicant(s): Bachmann, et al.
Title: Farnesyl Dibenzo(a)azepine, Processes for its Production
The Following, DUE _____ in the USPTO, was received by the PTO Mail Room on the date stamped hereon:

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| <ul style="list-style-type: none"><input type="checkbox"/> Cert. of Mailing by Express Mail (37 CFR 1.10)Express Mail Label No. <u>819329320395</u><input type="checkbox"/> Cert. of Mailing under 37 CFR 1.8(a)<input type="checkbox"/> Patent Application (<u>142</u> total pgs)<ul style="list-style-type: none"><input type="checkbox"/> Provisional or <input checked="" type="checkbox"/> Non-Provisional(<u>12</u> pgs) Specification (<u>1</u> pgs) Abstract,(<u>20</u> pgs) Claims (<u>73</u> # claims)<input type="checkbox"/> New Patent Application Transmittal<input type="checkbox"/> Provisional Patent Application Cover Sheet<input type="checkbox"/> Declaration and Power of Attorney<input type="checkbox"/> Application Data Sheet<input type="checkbox"/> Drawings <u>147</u> Sheet(s) (FIGS. <u>1</u>)<ul style="list-style-type: none"><input type="checkbox"/> Formal or <input checked="" type="checkbox"/> Informal<input type="checkbox"/> Assignment of _____<input type="checkbox"/> Recordation Cover Sheet Form PTO-1595<input type="checkbox"/> Information Disclosure Statement<input type="checkbox"/> Form PTO 1449 and Copies of Cited References | <ul style="list-style-type: none"><input type="checkbox"/> Response to Notice to File Missing Parts<input type="checkbox"/> Copy of Part 2 of NFMP<input type="checkbox"/> Diskette Containing Nucleotide and/or Amino Acid Sequence Listing<input type="checkbox"/> Priority Document(s) # _____<input type="checkbox"/> Amendment/Response<input type="checkbox"/> Petition for Extension of Time (x2)<input type="checkbox"/> Check in the amount of _____ Cher'k # _____<input type="checkbox"/> Transmittal of Formal Drawings<input type="checkbox"/> Motion/Opposition/Reply<input type="checkbox"/> Request for Cont'd Examination (RCE)<input type="checkbox"/> Notice of Appeal<input type="checkbox"/> Appeal Brief (x3)<input type="checkbox"/> Issue Fee Transmittal<input type="checkbox"/> Transmittal Letter (x2) |
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☐ Other Paper Copy of Sequence Listing, Statement Under
37 C.F.R. § 1.825(f) & (g)

MAILED January 21, 2004

SEQUENCE LISTING



<110> ECOPIA BIOSCIENCES INC.
Farnet, Chris
McAlpine, James
Zazopoulos, Emmanuel
Bachmann, Brian
Pirae, Mahmood

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<400> 2

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| Val | His | Asn | Leu | Asp | Asn | Ile | Pro | Ser | Ser | Pro | Ser | Thr | Ser | Gly | Gly | 1 | 5 | 10 | 15 |
| Ser | Leu | Pro | Ala | Gly | His | Arg | Ala | His | Val | Arg | Ala | Asp | Gly | Val | Arg | 20 | 25 | 30 | |
| Val | Val | Arg | Gly | Gly | Arg | Val | Val | Leu | Ser | Asp | Val | Ser | Val | Thr | Val | 35 | 40 | 45 | |
| Ser | Ala | Ala | Ser | Arg | Leu | Ala | Val | Val | Gly | Glu | Asn | Gly | Arg | Gly | Lys | 50 | 55 | 60 | |
| Thr | Thr | Leu | Leu | His | Val | Leu | Ala | Gly | Leu | Ile | Ala | Pro | Asp | Gln | Gly | 65 | 70 | 75 | 80 |
| Val | Val | Glu | Arg | Leu | Gly | Thr | Ile | Gly | Val | Ala | Arg | Gln | Asn | Leu | Glu | 85 | 90 | 95 | |
| Ser | Arg | His | Gly | Glu | Thr | Val | Gly | Thr | Leu | Val | Arg | Glu | Ala | Ile | Arg | 100 | 105 | 110 | |
| Glu | Ser | Glu | Arg | Ala | Leu | Arg | Ala | Leu | Asp | Glu | Ala | Thr | Ile | Ala | Leu | 115 | 120 | 125 | |
| Thr | Glu | Gly | Arg | Ala | Gly | Ala | Asp | Asp | Ala | Tyr | Ala | Ala | Ala | Leu | Asp | 130 | 135 | 140 | |
| Ala | Ala | Thr | Arg | Leu | Asp | Ala | Trp | Asp | Ala | Gln | Arg | Arg | Val | Asp | Val | 145 | 150 | 155 | 160 |
| Ala | Leu | Ala | Gly | Leu | Asp | Ala | Cys | Pro | Asp | Arg | Asp | Arg | Gln | Leu | Ala | 165 | 170 | 175 | |
| Thr | Leu | Ser | Val | Gly | Gln | Arg | Tyr | Arg | Val | Arg | Leu | Ala | Cys | Leu | Leu | 180 | 185 | 190 | |
| Gly | Ala | Arg | Val | Asp | Leu | Leu | Met | Leu | Asp | Glu | Pro | Thr | Asn | His | Leu | 195 | 200 | 205 | |
| Asp | Ala | Asp | Ser | Leu | Ala | Phe | Leu | Thr | Ala | Arg | Leu | Arg | Asp | His | Pro | 210 | 215 | 220 | |
| Gly | Gly | Val | Val | Leu | Val | Thr | His | Asp | Arg | Ala | Leu | Leu | Arg | Asp | Val | 225 | 230 | 235 | 240 |
| Ala | Thr | Glu | Phe | Leu | Asp | Leu | Asp | Pro | Ser | Ala | Asp | Gly | Arg | Pro | Arg | 245 | 250 | 255 | |
| Arg | Tyr | Ala | Gly | Asp | Tyr | Val | Ala | Trp | Gln | Asp | Gly | Arg | Arg | Arg | Asp | | | | |

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| Phe | Ala | His | Trp | Val | Arg | Asp | His | Glu | Ala | Gln | Gln | Ala | Glu | His | Gln |
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| Trp | Arg | Pro | Glu | Lys | Gly | His | Gly | Lys | His | Gln | Arg | Gln | Ser | Arg | Ala |
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| Pro | Gly | Leu | Val | Gln | Ala | Leu | Arg | Arg | Arg | Gln | Glu | Ala | Leu | Asp | Ala |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| His | Arg | Val | Thr | Val | Pro | Glu | Pro | Pro | Gln | Pro | Leu | Arg | Trp | Pro | Pro |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Leu | Asp | Thr | Arg | Ala | Gly | Leu | Pro | Ile | Leu | Arg | Cys | His | Asp | Val | Thr |
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| Val | Ala | Gly | Arg | Leu | Arg | Thr | Arg | Val | Thr | Leu | Thr | Leu | Asp | Gly | Gly |
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| Asp | Arg | Leu | Leu | Val | Thr | Gly | Pro | Asn | Gly | Ala | Gly | Lys | Ser | Thr | Leu |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Leu | Ser | Val | Leu | Ala | Gly | Asp | Leu | Thr | Pro | Ser | Thr | Gly | Glu | Val | Arg |
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| His | Leu | Ser | Gly | Ala | Arg | Val | Ala | Tyr | Leu | Gly | Gln | Glu | Val | Pro | Asp |
| | | | 420 | | | | 425 | | | | | | 430 | | |
| Trp | Pro | Pro | Ala | Leu | Leu | Ala | His | Asp | Leu | Tyr | Glu | Gln | His | Val | Gly |
| | 435 | | | | | 440 | | | | | 445 | | | | |
| Arg | Leu | Arg | Ser | Ser | Gly | Arg | Val | Gly | Ser | Gly | Thr | Ala | Leu | Pro | Leu |
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| Ser | Ala | Thr | Asn | Leu | Leu | Asp | Ala | Glu | Ala | Arg | Arg | Thr | Pro | Val | Gly |
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| Arg | Met | Ser | His | Gly | Gln | Gln | Arg | Arg | Leu | Asn | Leu | Ala | Leu | Arg | Leu |
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| Ala | Glu | Arg | Pro | Asp | Leu | Leu | Ile | Leu | Asp | Glu | Pro | Thr | Asn | His | Leu |
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| Ser | Ala | Pro | Leu | Val | Asp | Asp | Leu | Thr | Ala | Ala | Leu | Leu | Thr | Thr | Arg |
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| Ala | Ala | Val | Val | Val | Ala | Thr | His | Asp | Arg | Gln | Met | Leu | Gln | Asp | Leu |
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| Ala | Ala | Trp | Pro | Thr | Leu | Pro | Leu | Thr | Ala | Pro | Ala | Ala | Ser | Gly | Arg |
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<213> Micromonospora sp. strain 046-EC011

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Val Ala Glu Leu Ala Arg Gly Leu Ala Glu Glu Gly Leu Ile Arg Glu
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Thr Asn Gly Arg Ala Glu Leu Val Ser Arg Arg Ile Pro Arg Arg Val
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Asp Val Ser Arg Met Leu Gly Arg Ser Ser Ala Ala Leu Leu Pro Pro
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Val Asp Glu Ala Ile Ala Ser Gly Phe Val Val Ala Ala Glu His Gln
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Leu Ala Phe Gln Ser Asp Phe Leu Leu Arg Gly Ile Ile Glu Ser Ile
165 170 175
Pro Gly Pro Ala Arg Asp Ala Leu Arg Arg Glu Ala Met Ser Leu Ser
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Gly Arg Arg Arg Pro Ala Ala Asp Gln Asn Arg Arg Leu Asp Ala Ala
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| Arg Arg Asp Ala Glu Ala Cys Leu Val Leu Ala Asp Leu Leu Leu Gly 260 265 270 | | |
| Gly Glu Gly Gly Gly Pro Met Thr Glu Ala Ile Leu Arg Glu Arg Asp 275 280 285 | | |
| Ala Glu Ser Gly Asp Ala Ala Leu Ala Met Ala Leu Thr Ala Arg Ser 290 295 300 | | |
| Thr Gly Leu Trp Ser Ala Gly Lys Leu Ala Glu Gly Leu Lys Leu Gly 305 310 315 320 | | |
| Arg Ala Ala Val Arg Ala Gly Ala Glu Ala Glu Pro Val Trp Arg Leu 325 330 335 | | |
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| Leu Pro Ala Pro Ile Trp Thr Ala Ala Thr Ala Val Met Arg Ser Arg 370 375 380 | | |
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| Leu Ala Tyr Ala Val Leu Ser Thr Ala Ser Phe Tyr Met Gly Asp Leu 420 425 430 | | |
| Pro Ala Ala Ile Glu Tyr Leu Arg Arg Gly Gln Arg Asp Ala Asp Arg 435 440 445 | | |
| His Val Val Leu Asp Ser Val Gln Tyr Ser Trp Ala Glu Val Leu Ile 450 455 460 | | |
| Thr Val Lys Gln Glu Gly Pro Arg Ala Ala Ala Gln Leu Leu Ala Gly 465 470 475 480 | | |
| Lys His His Arg Leu Pro Thr Gln Arg Arg Leu Tyr Val Glu Val Pro 485 490 495 | | |
| Ser Ala Ala Ala Phe Leu Val Leu Leu Ala Arg Asp Val Asp Asp Arg 500 505 510 | | |
| Asp Leu Glu Arg Arg Val Leu Asp Thr Val Asn Gly Leu Ala Ala Asp | | |

| 515 | 520 | 525 |
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| Leu Ala Asn Ser Ala Pro Ala Ala Leu Ala Leu Ile Ile Val Gln Ser 545 550 555 560 | | |
| Arg Asp Pro Ile Ser Val Ala Leu Ala Thr Glu Glu Leu Ala Lys Leu 565 570 575 | | |
| Tyr Ala Ala Gln Ala Gln Ala Gly Gly Arg Pro Ala Thr Pro Ala Arg 580 585 590 | | |
| Ala Glu Glu Ala Ala Thr Pro Pro Ala Ser Cys Trp Ser Thr Leu Ser 595 600 605 | | |
| Asp Met Glu Gln Arg Ile Ala Tyr Leu Val Ser Val Gly Leu Thr Asn 610 615 620 | | |
| Arg Gln Ile Ala Lys Gln Val His Leu Ser Ala His Thr Val Asn Tyr 625 630 635 640 | | |
| His Leu Arg Lys Ile Tyr Arg Lys Leu Gly Phe Asn Thr Arg Ala Glu 645 650 655 | | |
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| cagaatcgcc ggttgagcgc ggcgcctacc gcgcgggtga gcgcgaecgg ggaggacgcc | 660 |
| accggatcct gttcccgggc gcaccgcctg ataatgaacg ggaacgcgaa ggccggcatt | 720 |
| cgcgctcgccg agggcggttct cgccggcccc gccgcgtcgc tcgctgcccg gcgtgacgcg | 780 |
| gaggcggtgc tgggtgctggc cgatctgctg ctccggcgggg agggcgggcg cccgatgacc | 840 |
| gaggcgatcc tgcgcgaacg cgacgccgag tccggtgacg ccgcactggc gatggcgctg | 900 |
| accgcccggc ccaccgggct gtggctcggc ggaagctgg cggagggcct gaagctggga | 960 |
| cgggcgggcg tgcggggcg cgcgaggcc gaaccgggtg ggcgtctgca cgcccagctc | 1020 |
| gcgctcgccg ggaaactcgc gaacctccgc gagttcgacg aggccgaggc gttgatcaac | 1080 |
| gaggcggaag cgggcctgcg cggactgccc gcgcgatct ggacggccgc gacggcggtg | 1140 |
| atgcggtccc ggttgctgct ccaggcgggg cggatcgggg aggcgcgtcg ggaggcggcg | 1200 |
| ctggccacca ccgcctgga gggggacgc gtgccgatgc tgcggcctct cgcctacgcg | 1260 |
| gtgctcagca ccgcctcctt ctacatgggg gacctgccc cgcgatcga gtacctcagg | 1320 |
| cgggggcagc gggacgcgga ccgccacgtg gtccctcgact cggtcagta ctcgtaggcg | 1380 |
| gaagtgcgtga tcacggtcaa gcaggaaggc ccggggggcg ccgccagct gctcgggggc | 1440 |
| aagcaccacc gcctgcccac gcagcgccgc ctctacgtcg aggtgccgag cgccgccgc | 1500 |
| ttcctggtcc tgctcgccc cgacgtggac gaccgtgacc tcgaacgcc cgctctcgac | 1560 |
| acggtcaacg ggctcgccgc ggacaacccc aggatccagg tcgtcagcct caccgccatg | 1620 |
| cacgcccacg cgctggcgaa cagcgctccg gccgccctgg cgctcatcat cgtgcagtca | 1680 |
| cgggacccga tctcggtggc gctggccacc gaggaactcg ccaagctcta cgccgcgcag | 1740 |
| gccagggcg ggggacggc ggcgacgcc gccgcgccg aggaggccgc cccccgccg | 1800 |
| gcgagctgct ggtcgaccct gtccgacatg gagcagcgga tcgcctacct ggtgagcgtg | 1860 |
| ggtctgacga accggcagat cgccaagcag gtccacctgt ccgcgcacac cgtcaactac | 1920 |
| cacctgcgga agatctaccg gaaactgggt ttcaacaccc gggccgagct ggcgcacgcc | 1980 |
| gcggccacgt actccggccg ggcggcgatc tactccatga gcggcgacca ggactggggc | 2040 |
| gccggatcca tgaccggcaa ggccagctga | 2070 |

<210> 6
<211> 895

<212> PRT

<213> Micromonospora sp. strain 046-ECO11

<400> 6

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20 25 30
Val Val Asp Gly Pro Phe Gly Ile Gly Lys Thr His Leu Leu Lys Val
35 40 45
Thr Gly Leu Glu Ala Ala Ala Arg Gly Leu Thr Val Val Ala Gly Arg
50 55 60
Ala Ser Val Thr Asp Gln Pro Val Pro Val His Leu Leu Val Asn Phe
65 70 75 80
Leu Arg His Ala Met Pro Gly Glu Ala Ala Val Glu Gln Leu Ala Leu
85 90 95
Pro Gly Ala Asn Pro Phe Trp Leu Ile Asp Arg Val Gly Asp Leu Val
100 105 110
Glu Val Ala Ala Arg Arg Arg Pro Leu Val Val Ala Leu Asp Asp Ala
115 120 125
Gln Arg Ile Asp Asp Val Ser Ala Leu Ala Leu Arg Gly Leu Val Pro
130 135 140
Arg Leu Ala Ser Ser Pro Val Leu Trp Leu Leu Ala Arg Arg Pro Val
145 150 155 160
Ala Ala Gly Ser Ile Ala Gln His Ala Val Asp Trp Leu Ala Glu His
165 170 175
Val Ala Val Arg Val Arg Leu Arg Glu Pro Gly Glu Glu Ala Val Ala
180 185 190
Asp Leu Cys Ala Gly Ile Leu Gly Ala Arg Pro Asp Ala Ser Val Leu
195 200 205
Arg Trp Ala Ala Arg Cys Gly Gly Asn Pro Lys Val Met Glu Ile Val
210 215 220
Phe Ser Ala Phe Ile Lys Ala Gly Gln Met Ile Ile Val Asp Gly Ala
225 230 235 240
Ala Ser Val Val Ser Asp Glu Leu Pro Asp Gly Val Leu Ala Ala Val
245 250 255
Arg Gly Leu Leu Glu Glu Leu Pro Pro Pro Leu Arg Arg Leu Leu Ala
260 265 270
Ala Gly Gly Arg Leu Gly His Thr Phe Pro Val Asp Arg Val Thr Gly

| 275 | | | | | 280 | | | | | 285 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Asp | Gly | Ser | Ala | Ala | Asp | Val | Ser | Ala | Ala | Ile | Asp | Glu | Ala |
| 290 | | | | | 295 | | | | | 300 | | | | | |
| Val | Arg | Val | Gly | Leu | Ile | Arg | Arg | Asp | Gly | Ala | Glu | Leu | Thr | Phe | Ala |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| His | Pro | Val | Leu | Gly | Glu | Ala | Leu | Arg | His | Ala | Ala | Tyr | Pro | Glu | Pro |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Glu | Arg | Ala | Glu | Pro | Gly | Ser | Ala | Pro | Ala | Pro | Ala | Ala | Gly | Asp | Pro |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Val | Arg | Arg | Gly | Arg | Pro | Asp | Pro | Arg | Pro | Gly | Thr | Pro | His | Ser | Pro |
| | | | 355 | | | | 360 | | | | | 365 | | | |
| Ala | Gly | Val | Arg | Val | Thr | Arg | Ser | Ala | Pro | Asp | Ala | Ala | Thr | Pro | Ala |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ala | Thr | Ala | Gly | Pro | Arg | Ser | Gly | Arg | Cys | Gly | Cys | Asp | Asp | Val | Ala |
| 385 | | | | 390 | | | | | 395 | | | | | | 400 |
| Ala | Ala | Ala | Val | Ser | His | Leu | Glu | Asn | Gly | Ser | Ala | Glu | Ala | Pro | Arg |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Ala | Leu | Ala | Arg | Ala | Leu | Arg | Leu | Leu | Ala | Gly | Ala | Gly | Arg | Ala | Ala |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Glu | Ala | Gly | Arg | Leu | Ala | Glu | Val | Met | Leu | Arg | Arg | Asp | Leu | Ala | Ala |
| | 435 | | | | | | 440 | | | | | 445 | | | |
| Asp | Val | Glu | Ala | Gln | Leu | Val | Leu | Glu | Leu | Gly | His | Gly | Met | Arg | Ala |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Ala | Gly | Ser | His | Arg | Leu | Ala | Ala | Gly | Phe | Leu | Arg | Arg | Thr | Gln | Ala |
| 465 | | | | 470 | | | | | 475 | | | | | 480 | |
| Arg | His | Asp | Val | Cys | Glu | Leu | Asp | Arg | Ala | Lys | Leu | Asp | Arg | Ala | Leu |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Ala | Asp | Thr | Thr | Lys | His | Leu | Gly | Gly | Ala | Ser | Ser | Ala | Glu | Leu | Glu |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Pro | Arg | His | Gln | Ser | Pro | Gly | Cys | Ala | Pro | Gly | Arg | Arg | Pro | Leu | Trp |
| | | | 515 | | | | 520 | | | | | 525 | | | |
| Thr | Trp | Leu | Val | Arg | Ala | Leu | Gly | Ala | Ala | Asp | Gln | Leu | Asp | Glu | Ala |
| 530 | | | | | | 535 | | | | | 540 | | | | |
| Gln | Ala | Val | Leu | Asp | Thr | Val | Arg | Pro | Leu | Ala | Gln | Glu | Pro | Ser | His |
| 545 | | | | 550 | | | | | | | 555 | | | | 560 |
| Thr | Gly | Ser | Glu | Ser | Leu | Trp | Arg | Gly | His | Arg | Ala | Glu | Leu | Leu | Ala |
| | | | | 565 | | | | 570 | | | | | | 575 | |
| Ala | Ala | Gly | Arg | Leu | Asp | Glu | Ala | Arg | Ala | Glu | Ala | Glu | Ala | Ala | Leu |

| 580 | | | | | 585 | | | | | 590 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ala | Ala | Asp | His | Ser | Arg | Pro | Gly | Asp | Cys | Val | Pro | Ala | Arg | Leu | |
| 595 | | | | | 600 | | | | | 605 | | | | | | |
| Val | Leu | Ala | His | Leu | Gly | Val | His | His | Gly | Asp | Leu | Ala | Thr | Ala | Ser | |
| 610 | | | | | 615 | | | | | 620 | | | | | | |
| Asp | Gln | Leu | Arg | Ala | Ala | Glu | Arg | Leu | Ala | Ser | Ala | Asp | Asp | Ser | Ala | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| Arg | Met | Asp | Trp | Ala | Leu | Ala | Arg | Phe | His | Ala | Ala | Ser | Gly | Arg | Pro | |
| 645 | | | | | 650 | | | | | 655 | | | | | | |
| Ala | Met | Met | Val | Gln | Thr | Leu | Ile | Asn | Val | Ala | Gly | Gln | Val | Ala | Pro | |
| 660 | | | | | 665 | | | | | 670 | | | | | | |
| Asp | Pro | Leu | Leu | Phe | Thr | Glu | Ala | Pro | Ala | Ala | Ala | Ala | Thr | Leu | Val | |
| 675 | | | | | 680 | | | | | 685 | | | | | | |
| Arg | Gln | Ala | Arg | Arg | Ala | Gly | Leu | Asp | Ala | Glu | Ala | Glu | Arg | Ala | Val | |
| 690 | | | | | 695 | | | | | 700 | | | | | | |
| Glu | Val | Ala | Arg | Arg | Val | Ala | Arg | Gly | Asn | Pro | Phe | Val | Gln | Ser | Leu | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Ala | Ala | Ala | Ala | Glu | His | Ala | Ala | Gly | Leu | Leu | Arg | Asp | Asp | Pro | Ala | |
| 725 | | | | | 730 | | | | | 735 | | | | | | |
| Ala | Leu | Leu | Arg | Ala | Ala | Asp | Leu | His | Arg | Leu | Ala | Gly | Arg | Thr | Leu | |
| 740 | | | | | 745 | | | | | 750 | | | | | | |
| Ala | Ala | Ala | Gly | Ala | Val | Glu | Asp | Ala | Ala | Arg | Ser | Thr | Arg | Asp | Arg | |
| 755 | | | | | 760 | | | | | 765 | | | | | | |
| Ala | Glu | Ala | Thr | Arg | Leu | Leu | Glu | Ala | Ala | Thr | Asp | Gly | Tyr | Arg | Glu | |
| 770 | | | | | 775 | | | | | 780 | | | | | | |
| Cys | Gly | Ala | Arg | Arg | Asp | Leu | Glu | Arg | Val | Glu | Ala | Glu | Leu | Arg | Gly | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Leu | Pro | Ala | His | Asn | Val | Arg | Pro | Leu | Val | Pro | Asp | Arg | Pro | Arg | Ser | |
| 805 | | | | | 810 | | | | | 815 | | | | | | |
| Gly | Trp | Glu | Ser | Leu | Thr | Ser | Ala | Glu | Leu | Arg | Val | Val | Arg | Ala | Ile | |
| 820 | | | | | 825 | | | | | 830 | | | | | | |
| Val | Asp | Gly | Met | Thr | Asn | Arg | Glu | Ala | Ala | Ser | Ser | Leu | Phe | Leu | Ser | |
| 835 | | | | | 840 | | | | | 845 | | | | | | |
| Pro | His | Thr | Val | Asp | Ser | His | Leu | Arg | Arg | Val | Phe | Ser | Lys | Leu | Asp | |
| 850 | | | | | 855 | | | | | 860 | | | | | | |
| Ile | Asn | Ser | Arg | Val | Glu | Leu | Thr | Arg | Cys | Phe | Ile | Ala | His | Glu | Ala | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |
| Val | Arg | Pro | Ala | Leu | Ala | Thr | Thr | Arg | Gln | Pro | Ala | Ser | Ala | Gly | | |

885

890

895

<210> 7

<211> 2688

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 7

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| ctcgacgcca ccatgcgagg atccgggggc tgcgtcgctg tcgacgggac gttcggcatc | 120 |
| ggcaagaccc acctgctgaa ggtcaccggc ctggaggcgg cggcccgagg gctgacagt | 180 |
| gtggccgggc gggcaagcgt caccgatcag ccggtgcccg tacacctgct cgtcaacttc | 240 |
| ctgcgccacg cgatgcccgg cgaagcgagg gtcgagcagc tcgccctgcc gggcgccaac | 300 |
| ccgttctggc tgatcgaccg ggtcggcgat ctggtcgagg tcgcgggcgg ccggcgccc | 360 |
| ctcgtggctg ccctggacga cggcagcgc atcgacgacg tcagcgccct ggccctgcgc | 420 |
| gggctcgtgc cgcgcctggc gtccctgcgc gtgctctggc tgctggccc cggccggctc | 480 |
| gccgcccggg cgatcgctca gcacgccgtc gactggctgg ccgagcacgt cgcggtacgg | 540 |
| gtacggctgc gcgagccggg cgaggaggcg gtggccgacc tgtgcgccc catcctcggc | 600 |
| gcccggccgg acgcctcgt cctgcgctgg gcccgcgct gcggcgga cccgaagggt | 660 |
| atggagatcg tcttcagcgc gttcatcaag gccggccaga tgatcatcgt ggacggggcg | 720 |
| gcgtcggctg tgtccgacga gctgcccgc ggtgtcctcg ccgccgttcg cgggctgctg | 780 |
| gaggagctgc cggcccgct gcggcgccct ctcgcccggc gcggccggct cggccacacg | 840 |
| tttcccgctc accgggtgac gggcctgctg gacggctcgg ccgccgacgt gtccgccgcg | 900 |
| atcgacgagg cgggtgcggg cgggctgata cgacgcgacg gcgaggagct gaccttcgcc | 960 |
| caccgggtgc tcggagaggc gcttcgccac gccgcgtacc cggaaaccgga gcgtgccgag | 1020 |
| cccggatccg cggcggcacc gggggcgagg gaccgggtcc ggcgcgggcg gccgatccg | 1080 |
| cggcccgagg cgcgccactc ccccgccggc gtacgcgtca cgcgctccgc gccggacgcg | 1140 |
| gccacgccc cgcgacggc ggggcccgc tcgggcccgt gcgggtgcga cgacgtggcg | 1200 |
| gcagccggcg tgtccacact ggagaacgga tccgccgagg cggcacgagc actggcccgt | 1260 |
| gcgctgcgcc tgctggccgg gggggggcgg gccgcgagg ccggccgcct cgcggagggtg | 1320 |
| atgctccgcc gcgacctgc gggggacgtc gaggcgcagc tcgtgctcga actgggacac | 1380 |
| gggatgcggg ccgcccgcag ccaccgcctg gcggccggct tcctgcgccg gacgcaggcc | 1440 |
| cggcacgacg tgtgcgagct ggaccgcgc aagctggacc gggcgctcgc ggacaccacg | 1500 |

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<210> 8

<211> 362

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 8

Met Thr Val Gly Tyr Leu Gly Thr Val Thr Asp Ser Ala Pro Val Asp
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Ala Ala Leu Arg Asp Phe Phe Ala Glu Arg Arg Ala Glu Ala Arg Glu
20 25 30

Leu Gly Asp Asp Phe Ala Ala Leu Val Ala Glu Leu Glu Ser Tyr Val
35 40 45

Leu Arg Gly Gly Lys Arg Ile Arg Pro Ala Phe Ala Trp Leu Gly Trp
 50 55 60
 Ile Gly Ala Gly Gly Asp Pro Glu Asp Pro Val Ala Thr Ala Val Leu
 65 70 75 80
 Asn Ala Cys Ala Gly Phe Glu Leu Leu His Ala Ser Gly Leu Ile His
 85 90 95
 Asp Asp Ile Ile Asp Ala Ser Gln Thr Arg Arg Gly His Pro Ala Ala
 100 105 110
 His Val Ala Tyr Ala Glu Arg His Arg Ala Arg Arg Phe Ser Gly Asp
 115 120 125
 Pro Gly Thr Phe Gly Thr Gly Thr Ala Ile Leu Ile Gly Asp Leu Val
 130 135 140
 Leu Ile Trp Ala Asp Val Leu Val Arg Ala Ser Gly Leu Pro Ala Asp
 145 150 155 160
 Ala His Val Arg Val Ser Pro Val Trp Ser Ala Val Arg Ser Glu Val
 165 170 175
 Met Tyr Gly Gln Leu Leu Asp Leu Ile Ser Gln Val Ser Arg Ser Glu
 180 185 190
 Asp Val Asp Ala Ala Leu Arg Ile Asn Gln Tyr Lys Thr Ala Ser Tyr
 195 200 205
 Thr Val Glu Arg Pro Leu Gln Phe Gly Ala Ala Ile Ala Gly Ala Asp
 210 215 220
 Asp Asp Leu Phe Ala Ala Tyr Arg Ala Phe Gly Ala Asp Val Gly Ile
 225 230 235 240
 Ala Phe Gln Leu Arg Asp Asp Leu Leu Gly Val Phe Gly Asp Pro Val
 245 250 255
 Val Thr Gly Lys Pro Ser Gly Asp Asp Leu Arg Glu Gly Lys Arg Thr
 260 265 270
 Val Leu Leu Ala Thr Ala Leu Lys Arg Ala Asp Glu Arg Asp Pro Asp
 275 280 285
 Ala Ala Ala Tyr Leu Arg Ala Lys Val Gly Thr Asp Leu Ala Asp Glu
 290 295 300
 Glu Ile Ala Arg Ile Arg Ala Ile Phe Arg Asp Val Gly Ala Val Glu
 305 310 315 320
 Glu Ile Glu Arg Gln Ile Ser Gln Arg Thr Asp Arg Ala Leu Ala Ala
 325 330 335
 Leu Glu Ala Ser Ser Ala Thr Ala Pro Ala Lys His Gln Leu Ala Asp
 340 345 350

Met Ala Ile Lys Ala Thr Gln Arg Ala Gln
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 <211> 1089
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 9
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 gtcgccgagc tggagagcta cgtcctgcgg ggccggaagc gcatccggcc cgccttcgcc 180
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 aaccagtaca agaccgcgtc gtacacggtg gagcggccac tgcagttcgg cgcggcgatc 660
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 gccagtgatg 1089

<210> 10
 <211> 354
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 10

Met Ser Thr Glu Pro Val Thr Val Val Ala Arg Gly Val Leu Asp Gly

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| Arg Gly Asp Gly Pro Gly Arg Leu Gly Thr Gly Arg Ala His Gly Lys | 20 | 25 | 30 |
| Ala Ile Leu Leu Gly Glu His Ala Val Val Tyr Gly Ala Pro Ala Leu | 35 | 40 | 45 |
| Ala Val Pro Val Pro Gln Leu Thr Ala Val Ala Lys Ala Arg Arg Ala | 50 | 55 | 60 |
| Gly Gly Asp Gly Gly Asp Glu Val Ser Phe Ala Ile Ala Gly Leu Glu | 65 | 70 | 75 |
| Ser Pro Glu Val Thr Ser Leu Pro Thr Asp Gly Leu Gln His Leu Val | 85 | 90 | 95 |
| Thr Glu Phe Arg Gln Arg Ala Ala Val Thr Glu Pro Met Arg Val Asp | 100 | 105 | 110 |
| Val Leu Val Asp Cys Ala Ile Pro Gln Gly Arg Gly Leu Gly Ser Ser | 115 | 120 | 125 |
| Ala Ala Cys Ala Arg Ala Ala Val Leu Ala Leu Ala Asp Ala Phe Asp | 130 | 135 | 140 |
| Arg Arg Leu Asp Ala Ala Thr Val Phe Asp Leu Val Gln Thr Ser Glu | 145 | 150 | 155 |
| Asn Val Ala His Gly Arg Ala Ser Gly Ile Asp Ala Leu Ala Thr Gly | 165 | 170 | 175 |
| Ala Thr Ala Pro Leu Ile Phe Arg Asn Gly Val Gly Arg Glu Leu Pro | 180 | 185 | 190 |
| Val Ala Met Ala Gly Ala Ala Arg Ala Ala Arg Gly Ser Gly Pro Ala | 195 | 200 | 205 |
| Gly Phe Asp Ala Val Leu Val Ile Ala Asp Ser Gly Val Ser Gly Ser | 210 | 215 | 220 |
| Thr Arg Asp Ala Val Glu Leu Leu Arg Gly Ala Phe Glu Arg Ser Pro | 225 | 230 | 235 |
| Arg Thr Arg Asp Glu Phe Val Ser Arg Val Thr Ser Leu Thr Glu Ala | 245 | 250 | 255 |
| Ala Ala His Asp Leu Leu Gln Gly Arg Val Ala Asp Phe Gly Ala Arg | 260 | 265 | 270 |
| Leu Thr Glu Asn His Arg Leu Leu Arg Glu Val Gly Ile Ser Thr Glu | 275 | 280 | 285 |
| Arg Ile Asp Arg Met Val Asp Ala Ala Leu Ala Ala Gly Ser Pro Gly | 290 | 295 | 300 |
| Ala Lys Ile Ser Gly Gly Gly Leu Gly Gly Cys Met Ile Ala Leu Ala | | | |

| | | | |
|---|-----|-----|-----|
| 305 | 310 | 315 | 320 |
| Arg Asp Arg Gln Glu Ser Ala Ala Val Val Arg Ser Val Gln Gln Ala | | | |
| 325 | 330 | 335 | |

| |
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| Gly Ala Val Arg Thr Trp Thr Val Pro Met Gly Arg Phe Thr Gly His |
| 340 345 350 |

Asp Asp

<210> 11
 <211> 1065
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 11

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| ccgggcccgc tcggcaccgg ccgcgcccac ggcaaggcca tcctgctggg cgaacacgcc | 120 |
| gtcgtgtacg gcgctccggc gctcgccgtc ccggtgccgc aactgaccgc cgtggccaag | 180 |
| gcgcggcggg ccggcgggca cggcgggcag gaggtctcct tcgccatcgc cgggctggag | 240 |
| agcccggagg tgacgtcgct tccgaccgac ggcctgcaac atctggtgac ggagttccgg | 300 |
| cagcggggccg ccgtcaccga gccgatgcgc gtcgacgtgc tcgtggactg cgccatcccg | 360 |
| cagggccggg ggctcgggtc gagcgccgdc tgcgcccgcg ccgcggtgct ggcctcgcg | 420 |
| gacgcgttcg accgccgcct cgacgccgcc acggtgttcg atctggtgca gacctcggag | 480 |
| aacgtggcgc acggccgggc cagcggcatc gacgccctgg ccaccggtgc gaccgcgccg | 540 |
| ctgatcttcc gcaacggcgt gggccgggaa ctgccggtcg ccatggcggg cgccgcgcgt | 600 |
| gccgcgcgag ggtcggggcc ggccggcttc gacgcggtgc tcgtcatcgc cgacagcggc | 660 |
| gtcagcggca gcacccggga cgcggtggag ctgctgcggg gtgccttcga gcgctccccg | 720 |
| cgcacgcgcg acgagttcgt cagccgggtg accagcctga ccgaggcggc ggcgcacgac | 780 |
| ctgctccagg gccgggtcgc cgacttcggc gcgcggctga ccgagaacca ccggctgttg | 840 |
| cgcgaggtcg gcatcagcac cgaacggatc gaccggatgg tcgacgccgc gctcgcggcg | 900 |
| ggcagccccg gcgccaagat cagcggcggt ggcctgggcg gctgcatgat cgcactggcc | 960 |
| cgggaccgcc aggaatccgc ggcggtggtg cggagcgtcc agcaggccgg cgccgtccgc | 1020 |
| acctggaccg tcccgatggg gaggttcacc ggccatgacg actga | 1065 |

<210> 12
 <211> 346
 <212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 12

Met Thr Thr Asp His Arg Ala Glu Pro Ser Glu Pro Ala Leu Asp Arg
1 5 10 15
Pro Ala Thr Ala Val Ala His Pro Asn Ile Ala Leu Ile Lys Tyr Trp
20 25 30
Gly Lys Arg Asp Glu Gln Leu Met Ile Pro Tyr Ala Asp Ser Leu Ser
35 40 45
Met Thr Leu Asp Val Phe Pro Thr Thr Thr Thr Val Arg Ile Asp Ser
50 55 60
Gly Ala Ala Ala Asp Glu Val Val Leu Asp Gly Ser Pro Ala Asp Gly
65 70 75 80
Glu Arg Arg Gln Arg Val Val Thr Phe Leu Asp Leu Val Arg Lys Leu
85 90 95
Ala Gly Arg Thr Glu Arg Ala Cys Val Asp Thr Arg Asn Ser Val Pro
100 105 110
Thr Gly Ala Gly Leu Ala Ser Ser Ala Ser Gly Phe Ala Ala Leu Ala
115 120 125
Leu Ala Gly Ala Ala Ala Tyr Gly Leu Asp Leu Asp Thr Thr Ala Leu
130 135 140
Ser Arg Leu Ala Arg Arg Gly Ser Val Ser Ala Ser Arg Ser Val Phe
145 150 155 160
Gly Gly Phe Ala Met Cys His Ala Gly Pro Gly Ala Gly Thr Ala Ala
165 170 175
Asp Leu Gly Ser Tyr Ala Glu Pro Val Pro Val Ala Pro Leu Asp Val
180 185 190
Ala Leu Val Ile Ala Ile Val Asp Ala Gly Pro Lys Ala Val Ser Ser
195 200 205
Arg Glu Gly Met Arg Arg Thr Val Arg Thr Ser Pro Leu Tyr Gln Ser
210 215 220
Trp Val Ala Ser Gly Arg Ala Asp Leu Ala Glu Met Arg Ala Ala Leu
225 230 235 240
Leu Gln Gly Asp Leu Asp Ala Val Gly Glu Ile Ala Glu Arg Asn Ala
245 250 255
Leu Gly Met His Ala Thr Met Leu Ala Ala Arg Pro Ala Val Arg Tyr
260 265 270
Leu Ala Pro Val Thr Val Ala Val Leu Asp Ser Val Leu Arg Leu Arg
275 280 285

Ala Asp Gly Val Ser Ala Tyr Ala Thr Met Asp Ala Gly Pro Asn Val
 290 295 300

Lys Val Leu Cys Arg Arg Ala Asp Ala Asp Arg Val Ala Asp Thr Leu
 305 310 315 320

Arg Asp Ala Ala Pro Ser Cys Ala Val Val Val Ala Gly Pro Gly Pro
 325 330 335

Ala Ala Arg Pro Asp Pro Gly Ser Arg Pro
 340 345

<210> 13

<211> 1041

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 13

| | |
|---|------|
| atgacgactg accaccgggc ggagccgtcc gagccggcgc tcgaccggcc cgcgaccgcc | 60 |
| gtggcccatc cgaacatcgc gctgatcaag tactggggca agcgcgacga gcagctgatg | 120 |
| atcccgtagc ccgacagcct gtcgatgacg ctcgacgtct tcccgaccac caccaccgtc | 180 |
| cggatcgaca gcggcgcggc ggccgacgag gtcgtcctcg acggctcgcc cgccgacggc | 240 |
| gaacggcgac agcgcgtcgt caccttctcg gacctggtac gcaagctggc cgggcgcacg | 300 |
| gaacggggct gcgtcgacac ccgcaactcc gtgcccaccg gcgcccggct ggcgtcctcg | 360 |
| gcgagcggat tcgccgccct cgccctcgcc ggcgcgcgcg cgtacggcct cgacctggac | 420 |
| accaccgcgc tgtccgcct ggcccggcgg ggatccgtgt cggcctcccg gtcggtcttc | 480 |
| ggcggcttcg cgatgtgcca cgcaggcccc ggcgccggga ccgccgcgga cctcggctcc | 540 |
| tacgccgagc cggtgcccgt cgcgccctc gacgtcgcgc tggatgatgc gatcgtcgac | 600 |
| gccggggcca aggcggtgtc gagccgcgag gggatgcggc gaaccgtccg gacctccccg | 660 |
| ctctatcagt cgtgggtcgc ctccggccgc gccgacctgg ccgagatgcg ggccgcgctg | 720 |
| ctccagggag acctggacgc ggtcggcgag atcgccgaac gcaacgccct cggcatgcac | 780 |
| gccaccatgc tggccgcccg gccggcgggt cgctacctgg cgccggtcac tgtcgccgtg | 840 |
| ctcgacagcg tgctgcgcct gcgcgccgac ggcgtctccg cctacgccac gatggacgcg | 900 |
| ggaccgaacg tcaaggtgct ctgccgccgc gcggacgccg accgggtcgc cgacaccctg | 960 |
| cgcgacgccg cgccgagctg cgccgtggtc gtcgccggac cggggccggc ggcccgcccg | 1020 |
| gaccggggca gccggccgtg a | 1041 |

<210> 14

<211> 369
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 14

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Gly | Pro | Gly | Ala | Val | Arg | Arg | His | Ala | Pro | Gly | Lys | Leu | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ala | Gly | Glu | Tyr | Ala | Val | Leu | Glu | Pro | Gly | His | Pro | Ala | Leu | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ala | Val | Asp | Arg | Gly | Val | Asp | Val | Thr | Val | Ser | Gly | Ala | Asp | Ala |
| | | | 35 | | | | | 40 | | | | 45 | | | |
| His | Leu | Val | Val | Asp | Ser | Asp | Leu | Cys | Pro | Glu | Gln | Ala | Cys | Leu | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Trp | Gln | Asp | Gly | Arg | Leu | Val | Gly | Ala | Gly | Asp | Gly | Gln | Pro | Ala | Pro |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asp | Ala | Leu | Gly | Ala | Val | Val | Ser | Ala | Ile | Glu | Val | Val | Gly | Glu | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Thr | Gly | Arg | Gly | Leu | Arg | Pro | Leu | Pro | Met | Arg | Val | Ala | Ile | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Arg | Leu | His | Arg | Asp | Gly | Thr | Lys | Phe | Gly | Leu | Gly | Ser | Ser | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Val | Thr | Val | Ala | Thr | Val | Thr | Ala | Val | Ala | Ala | Tyr | His | Gly | Val |
| | | 130 | | | | | 135 | | | | 140 | | | | |
| Glu | Leu | Ser | Leu | Glu | Ser | Arg | Phe | Arg | Leu | Ala | Met | Leu | Ala | Thr | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Asp | Gly | Ala | Asp | Ala | Ser | Gly | Gly | Asp | Leu | Ala | Ala | Ser | Val | Trp |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Gly | Gly | Trp | Ile | Ala | Tyr | Gln | Ala | Pro | Asp | Arg | Ala | Ala | Val | Arg | Glu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Met | Ala | Arg | Arg | Arg | Gly | Val | Glu | Glu | Thr | Met | Arg | Ala | Pro | Trp | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gly | Leu | Arg | Val | Arg | Arg | Leu | Pro | Pro | Pro | Arg | Gly | Leu | Ala | Leu | Glu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Gly | Trp | Thr | Gly | Glu | Pro | Ala | Ser | Ser | Ser | Ser | Leu | Thr | Gly | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Leu | Ala | Ala | Ser | Arg | Trp | Arg | Gly | Ser | Pro | Ala | Arg | Trp | Ser | Phe | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ser | Arg | Ser | Gln | Glu | Cys | Val | Arg | Thr | Ala | Ile | Asp | Ala | Leu | Glu | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |

Gly Asp Asp Gln Glu Leu Leu His Gln Val Arg Arg Ala Arg His Val
 275 280 285
 Leu Ala Glu Leu Asp Asp Glu Val Arg Leu Gly Ile Phe Thr Pro Arg
 290 295 300
 Leu Thr Ala Leu Cys Asp Ala Ala Glu Thr Val Gly Gly Ala Ala Lys
 305 310 315 320
 Pro Ser Gly Ala Gly Gly Gly Asp Cys Gly Ile Ala Leu Leu Asp Ala
 325 330 335
 Thr Ala Ala Thr Arg Thr Ala Arg Leu Arg Glu Gln Trp Ala Ala Ala
 340 345 350
 Gly Val Leu Pro Met Pro Ile Gln Val His Gln Thr Asn Gly Ser Ala
 355 360 365

Arg

<210> 15
 <211> 1110
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 15
 gtgaccggcc cgggcgccgt gcgccgccac gcgccgggca agctgttcgt cgccggtgag 60
 tacgcggtgc tggagccggg ccaccggcg ctgctggtgg cggtcgacag gggagtggac 120
 gtcaccgtct cgggcgccga cgcccacctc gttgtcgact ccgacctctg cccggagcag 180
 gcgtgcctgc ggtggcagga cggccggctc gtcggcgcg ggcacgggca gccggcgccc 240
 gacgcctcgc gcgccgtggt ctggcgatc gaggtggtcg gcgaactcct gaccggacga 300
 gggctgcgcc cgctgcccat gcgggtggcg atcaccagcc ggctgcaccg cgacggcacg 360
 aagttcggcc tcgggtcgag cggggcggtg acagtcgcca cggtgaccgc agtggccgcg 420
 taccacgggg tggagctgtc gtcgaatcg cggttccggc tggcgatgct ggcgacggtg 480
 cgtgacggcg ccgacgcctc cggcgggtgat ctggccgcga gcgtctgggg cggttgatc 540
 gcctaccagg cggccgaccg cgcgccgtg cgcgagatgg cgcggcgggc cggcgctcag 600
 gagacgatgc gcgcgcctg gccgggcctg cgggtccggc ggctgccacc accgcgtggc 660
 ctcgcgctgg aggtgggctg gaccggcgag ccggcgagca gcagctcgtt gaccgggcg 720
 ctggccgcct cccggtggcg gggcagccc ggcgggtgga gcttcaccag ccgtagccag 780
 gagtgtgtgc gtaccgcat cgacgcgctg gagcggggcg acgaccagga actgctgcac 840
 caggtccggc gggcccgga cgtgcttgcc gagctggacg acgaggtccg gctcgggatc 900

ttcaccccc ggctgacggc gctgtgacgac gccgccgaga ccgtcggcgg cgccggccaaa 960
ccgtccggcg ccggtggcgg ggactgcggc atcgcggtgc tggacgccac cgccgcgacg 1020
cggaccgcgc ggctgcgcga gcagtggggc gccgccgggg tgctcccat gccgatccag 1080
gtccatcaga cgaacgggag cgcgcatga 1110

<210> 16
<211> 360
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 16

Met Ile Ala Asn Arg Lys Asp Asp His Val Arg Leu Ala Ala Glu Gln
1 5 10 15

Gln Gly Arg Leu Gly Gly His His Glu Phe Asp Asp Val Ser Phe Val
20 25 30

His His Ala Leu Ala Gly Ile Asp Arg Ser Asp Val Ser Leu Ala Thr
35 40 45

Ser Phe Gly Gly Ile Asp Trp Pro Val Pro Leu Cys Ile Asn Ala Met
50 55 60

Thr Gly Gly Ser Thr Lys Thr Gly Leu Ile Asn Arg Asp Leu Ala Ile
65 70 75 80

Ala Ala Arg Glu Thr Gly Val Pro Ile Ala Thr Gly Ser Met Ser Ala
85 90 95

Tyr Phe Ala Asp Glu Ser Val Ala Glu Ser Phe Ser Val Met Arg Arg
100 105 110

Glu Asn Pro Asp Gly Phe Ile Met Ala Asn Val Asn Ala Thr Ala Ser
115 120 125

Val Glu Arg Ala Arg Arg Ala Val Asp Leu Met Arg Ala Asp Ala Leu
130 135 140

Gln Ile His Leu Asn Thr Ile Gln Glu Thr Val Met Pro Glu Gly Asp
145 150 155 160

Arg Ser Phe Ala Ala Trp Gly Pro Arg Ile Glu Gln Ile Val Ala Gly
165 170 175

Val Gly Val Pro Val Ile Val Lys Glu Val Gly Phe Gly Leu Ser Arg
180 185 190

Glu Thr Leu Leu Arg Leu Arg Asp Met Gly Val Arg Val Ala Asp Val
195 200 205

Ala Gly Arg Gly Gly Thr Asn Phe Ala Arg Ile Glu Asn Asp Arg Arg
210 215 220

Asp Ala Ala Asp Tyr Ser Phe Leu Asp Gly Trp Gly Gln Ser Thr Pro
 225 230 235 240
 Ala Cys Leu Leu Asp Ala Gln Gly Val Asp Leu Pro Val Leu Ala Ser
 245 250 255
 Gly Gly Ile Arg Asn Pro Leu Asp Val Val Arg Gly Leu Ala Leu Gly
 260 265 270
 Ala Gly Ala Ala Gly Val Ser Gly Leu Phe Leu Arg Thr Leu Leu Asp
 275 280 285
 Gly Gly Val Pro Ala Leu Leu Ser Leu Leu Ser Thr Trp Leu Asp Gln
 290 295 300
 Ile Glu Ala Leu Met Thr Ala Leu Gly Ala Arg Thr Pro Ala Asp Leu
 305 310 315 320
 Thr Arg Cys Asp Leu Leu Ile Gln Gly Arg Leu Ser Ala Phe Cys Ala
 325 330 335
 Ala Arg Gly Ile Asp Thr His Arg Leu Ala Thr Arg Ser Gly Ala Thr
 340 345 350
 His Glu Met Ile Gly Gly Ile Arg
 355 360

<210> 17
 <211> 1083
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 17
 atgatcgcca accgcaagga cgaccacgtc cggctcgccg ccgagcagca gggccggctc 60
 ggcggtcacc acgagttcga cgacgtgtcc ttcgtgcacc acgccctggc cggcacgcac 120
 cggtcgcacg tctcgttggc cagctcgttc ggccggcatcg actggccggg gccgctgtgc 180
 atcaacgcga tgaccggcgg cagcaccaag accggcctga tcaaccggga cctggcgatc 240
 gcggcccggg agaccggcgt accgatcgcc accgggtcga tgagcgccta cttcgccgac 300
 gagtcggtgg ccgagagttt cagcgtgatg cgccgggaga accccgacgg gttcatcatg 360
 gccaacgtca acgccaccgc ctccgtcgaa cgggcccggc gggctgtcga cctgatgcgg 420
 gccgacgcgc tgcagatcca cctgaacacc atccaggaga cggatgatgcc ggagggggac 480
 cggtcgttcg ccgcctgggg gccgcggatc gaacagatcg tcgccggcgt cggtgtgccg 540
 gtgatcgtca aggaggtcgg cttcgggctc agccgcgaaa cgctgctgcg gctgcgggac 600
 atgggcgtcc ggggtggcga cgtcgccggc cgccggcgga cgaacttcgc gcgcatcgag 660
 aacgaccggc gggacgccgc cgactactcc ttctcgacg ggtggggaca gtcgacaccc 720

gcctgcctgc tggacgccca gggcgtggac ctgcccgctgc tggcctccgg cggcatccgc 780
aaccgcgtcg acgtggtccg cgggctggcg ctccggcgccg gcgcggccgg ggtgtccgga 840
ctgttctctgc gcacgtcctt ggacggcggc gtgccggcgc tgctgtcgt gctgtccacc 900
tggctcgacc agatcgaagc cctgatgacc gccctgggcg cgcggacccc ggccgacctg 960
accgcgtcgc acctgctgat ccagggtcgg ctgagcgcgt tctgcgcggc ccggggcatc 1020
gacaccacc gcctcgccac ccgttccggc gccaccacg agatgatcgg aggcattcga 1080
tga 1083

<210> 18
<211> 351
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Asp | Ala | Ile | Ala | Gly | Val | Pro | Met | Lys | Trp | Val | Gly | Pro | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Ile | Ser | Gly | Asn | Val | Ala | Gln | Ile | Glu | Thr | Glu | Val | Pro | Leu | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Tyr | Glu | Ser | Pro | Leu | Trp | Pro | Ser | Val | Gly | Arg | Gly | Ala | Lys | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Arg | Met | Val | Glu | Ala | Gly | Ile | Val | Ala | Thr | Leu | Val | Asp | Glu | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Met | Thr | Arg | Ser | Val | Phe | Val | Arg | Ala | Lys | Asp | Ala | Gln | Thr | Ala | Tyr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Ala | Ser | Leu | Glu | Val | Asp | Ala | Arg | Phe | Asp | Glu | Leu | Arg | Asp | Ile |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Arg | Thr | Cys | Gly | Arg | Phe | Val | Glu | Leu | Ile | Gly | Phe | His | His | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Thr | Ala | Asn | Leu | Leu | Phe | Leu | Arg | Phe | Ser | Phe | Thr | Thr | Gly | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Ser | Gly | His | Asn | Met | Ala | Thr | Leu | Ala | Ala | Asp | Ala | Leu | Leu | Lys |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| His | Ile | Leu | Asp | Thr | Ile | Pro | Gly | Ile | Ser | Tyr | Gly | Ser | Ile | Ser | Gly |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | |
| Asn | Tyr | Cys | Thr | Asp | Lys | Lys | Ala | Thr | Ala | Ile | Asn | Gly | Ile | Leu | Gly |
| | | | 165 | | | | | 170 | | | | | | 175 | |
| Arg | Gly | Lys | Asn | Val | Val | Thr | Glu | Leu | Val | Val | Pro | Arg | Glu | Ile | Val |

| | | |
|---|-----|-----|
| 180 | 185 | 190 |
| His Asp Ser Leu His Thr Thr Ala Ala Ala Ile Ala Gln Leu Asn Val | | |
| 195 | 200 | 205 |
| His Lys Asn Met Ile Gly Thr Leu Leu Ala Gly Gly Ile Arg Ser Ala | | |
| 210 | 215 | 220 |
| Asn Ala His Tyr Ala Asn Met Leu Leu Gly Phe Tyr Leu Ala Thr Gly | | |
| 225 | 230 | 235 |
| Gln Asp Ala Ala Asn Ile Val Glu Gly Ser Gln Gly Val Thr Val Ala | | |
| 245 | 250 | 255 |
| Glu Asp Arg Asp Gly Asp Leu Tyr Phe Ser Cys Thr Leu Pro Asn Leu | | |
| 260 | 265 | 270 |
| Ile Val Gly Thr Val Gly Asn Gly Lys Gly Leu Gly Phe Val Glu Glu | | |
| 275 | 280 | 285 |
| Asn Leu Glu Arg Leu Gly Cys Arg Ala Ser Arg Asp Pro Gly Glu Asn | | |
| 290 | 295 | 300 |
| Ala Arg Arg Leu Ala Val Ile Ala Ala Ala Thr Val Leu Cys Gly Glu | | |
| 305 | 310 | 315 |
| Leu Ser Leu Leu Ala Ala Gln Thr Asn Pro Gly Glu Leu Met Arg Ala | | |
| 325 | 330 | 335 |
| His Val Arg Leu Glu Arg Pro Thr Glu Thr Thr Lys Ile Gly Ala | | |
| 340 | 345 | 350 |

<210> 19

<211> 1056

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 19

| | |
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| atgaacgacg c gatcgccg tgtgcccattg aaatgggtag gtcccgtgcg gatctcggga | 60 |
| aacgtggcgc agatcgagac ggaggttccg ctcgccacgt acgagtcgcc gctctggccg | 120 |
| tccgtcggcc ggggcgcgaa gatctcccgg atggtcgagg cgggcatcgt cgccacgctc | 180 |
| gtcgacgagc gcatgaccgc ctcggtgttc gtgcgcgcca aggacgcgca gaccgcctac | 240 |
| ctggcctcgc ttgaggtcga cgcgcggttc gacgaactgc gtgacatcgt gcgcacctgc | 300 |
| ggcaggttcg tcgagctgat cgggttccac cagagatca ccgcgaacct gctgttcctg | 360 |
| cggttcagtt tcaccaccgc cgacgcgtcc gggcacaaca tggcgacgct ggccgccgac | 420 |
| gcgctgctga agcacatcct ggacaccatt cggggcatct cgtacggctc gatctcgggc | 480 |
| aactactgca ccgacaagaa ggccaccgcg ataaacggca ttctcggccg gggcaagaac | 540 |
| gtggtcaccg agctggtcgt gccgcgggag atcgccacg acagcctgca cacgacggcg | 600 |

gcggcgatcg cccagctgaa cgtgcacaag aacatgatcg gcacgttgct cgccggcggt 660
atccgctcgg ccaacgcccc ctacgcgaac atgctgctcg ggttctacct ggccacgggt 720
caggacgccg cgaacatcgt cgaggggtcc caggggcgtga cggtcgccga ggaccgcgac 780
ggcgacctct acttctcctg cacgctgccc aacctgatcg tgggcaccgt cggcaacggc 840
aaggggctcg gcttcgtcga ggagaacctg gagcgggtcg gctgccgcgc ctgcggtgat 900
ccgggcgaga acgcccggcg gctcgcggtc atcgcggccg cgacgggtgct ctgcggcgag 960
ctgtccctgc tcgccgcgca gaccaacctg ggcgagctga tgcgggcgca cgtccggctc 1020
gaacgcccga ccgagaccac gaagatcgga gcctga 1056

<210> 20
<211> 391
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 20

Met Ala Glu Arg Pro Ala Val Gly Ile His Asp Leu Ser Ala Ala Thr
1 5 10 15

Ala His His Val Leu Thr His Glu Thr Leu Ala Ala Ser Asn Gly Ala
20 25 30

Asp Val Ala Lys Tyr His Arg Gly Ile Gly Leu Arg Ala Met Ser Val
35 40 45

Pro Ala Pro Asp Glu Asp Ile Val Thr Met Ala Ala Ala Ala Ala Ala
50 55 60

Pro Val Val Ala Arg His Gly Thr Asp Arg Ile Arg Thr Val Val Phe
65 70 75 80

Ala Thr Glu Ser Ser Val Asp Gln Ala Lys Ala Ala Gly Ile His Val
85 90 95

His Ser Leu Leu Gly Leu Pro Ser Ala Thr Arg Val Val Glu Leu Lys
100 105 110

Gln Ala Cys Tyr Gly Gly Thr Ala Gly Leu Gln Phe Ala Ile Gly Leu
115 120 125

Val His Arg Asp Pro Ser Gln Gln Val Leu Val Ile Ala Ser Asp Val
130 135 140

Ser Lys Tyr Ala Leu Gly Glu Pro Gly Glu Ala Thr Gln Gly Ala Ala
145 150 155 160

Ala Val Ala Met Leu Val Gly Ala Asp Pro Ala Leu Val Arg Val Glu
165 170 175

Asp Pro Ser Gly Met Phe Thr Ala Asp Val Met Asp Phe Trp Arg Pro
 180 185 190
 Asn Tyr Arg Thr Thr Ala Leu Val Asp Gly His Glu Ser Ile Ser Ala
 195 200 205
 Tyr Leu Gln Ala Leu Glu Gly Ser Trp Lys Asp Tyr Thr Glu Arg Gly
 210 215 220
 Gly Arg Thr Leu Asp Glu Phe Gly Ala Phe Cys Tyr His Gln Pro Phe
 225 230 235 240
 Pro Arg Met Ala Asp Lys Ala His Arg His Leu Leu Asn Tyr Cys Gly
 245 250 255
 Arg Asp Val Asp Asp Ala Leu Val Ala Gly Ala Ile Gly His Thr Thr
 260 265 270
 Ala Tyr Asn Ala Glu Ile Gly Asn Ser Tyr Thr Ala Ser Met Tyr Leu
 275 280 285
 Gly Leu Ala Ala Leu Leu Asp Thr Ala Asp Asp Leu Thr Gly Arg Thr
 290 295 300
 Val Gly Phe Leu Ser Tyr Gly Ser Gly Ser Val Ala Glu Phe Phe Ala
 305 310 315 320
 Gly Thr Val Val Pro Gly Tyr Arg Ala His Thr Arg Pro Asp Gln His
 325 330 335
 Arg Ala Ala Ile Asp Arg Arg Gln Glu Ile Asp Tyr Ala Thr Tyr Arg
 340 345 350
 Glu Leu His Glu His Ala Phe Pro Val Asp Gly Gly Asp Tyr Pro Ala
 355 360 365
 Pro Glu Val Thr Thr Gly Pro Tyr Arg Leu Ala Gly Leu Ser Gly His
 370 375 380
 Lys Arg Val Tyr Glu Pro Arg
 385 390

<210> 21

<211> 1176

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 21

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| atggccgaga gacccgccgt cggcatccac gacctgtccg ccgcgacggc gcatcacgtg | 60 |
| ctgacacacg agaccctggc cgcgagcaac ggcgccgacg tggccaagta ccaccgtggc | 120 |
| atcgggctgc gggcgatgag cgtgccccgcc ccggacgagg acatcgtgac gatggctgct | 180 |
| gccgccgccg cgccggtggt cgccccccac ggcaccgacc ggatccggac cgtcgtgttc | 240 |

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gccacggagt cgtcggtcga ccaggcgaag gcgcccgga tacacgtcca ctccctgctc 300
ggcctccct cggccaccg ggtggtcgag ctgaagcagg cctgctacgg cggtagcgcg 360
ggactgcagt tcgccatcgg cctggtgcac cgtgaccgt cgcagcaggt cctggtgatc 420
gccagcgacg tgtcgaagta cgcgctgggt gagcccgcg aggcgaccca gggcgccg 480
gcggtcgcca tgctcgtcgg cgcggaccg gcgctggtac gcgtcgagga cccgtcgggc 540
atgttcaccg ccgacgtcat ggacttctgg cggccgaact accgcaccac cgccctggtc 600
gacgggcacg agtccatctc cgcctacctg caggcgctgg agggctcgtg gaaggactac 660
accgagcgcg gcggtcgcac cctggacgag ttcggcgctg tctgctacca ccagccgttc 720
ccgaggatgg ccgacaaggc gcaccggcac ctgctcaact actgcggcg cgacgtcgac 780
gacgcgctgg tggccggggc catcgggcac accaccgct acaacgccga gatcggcaac 840
agctacacgg cgtcgatgta tctcgggctc gcggcactgc tcgacaccgc cgacgacctg 900
accggccgga ccgctcggtt cctcagctac gggctccgga gcgtcgccga gttcttcgcc 960
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gaccggcggc aggagatcga ctacgcgacg taccgggagt tgcacgagca cgccttcccg 1080
gtcgacggcg gcgactatcc ggcgccggag gtgaccaccg ggccgtaccg gctggccggg 1140
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```

<210> 22
<211> 290
<212> PRT
<213> Micromonospora sp. strain 046-EC011

```

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<400> 22
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```

Val Ala Glu Leu Tyr Ser Thr Ile Glu Glu Ser Ala Arg Gln Leu Asp
1           5           10          15

```

```

Val Pro Cys Ser Arg Asp Arg Val Trp Pro Ile Leu Ser Ala Tyr Gly
20          25          30

```

```

Asp Ala Phe Ala His Pro Glu Ala Val Val Ala Phe Arg Val Ala Thr
35          40          45

```

```

Ala Leu Arg His Ala Gly Glu Leu Asp Cys Arg Phe Arg Thr His Pro
50          55          60

```

```

Asp Asp Arg Asp Pro Tyr Ala Ser Ala Leu Ala Arg Gly Leu Thr Pro
65          70          75          80

```

```

Arg Thr Asp His Pro Val Gly Ala Leu Leu Ser Glu Val His Arg Arg
85          90          95

```

Cys Pro Val Glu Ser His Gly Ile Asp Phe Gly Val Val Gly Gly Phe
 100 105 110
 Lys Lys Ile Tyr Ala Ala Phe Ala Pro Asp Glu Leu Gln Val Ala Thr
 115 120 125
 Ser Leu Ala Gly Ile Pro Ala Met Pro Arg Ser Leu Ala Ala Asn Ala
 130 135 140
 Asp Phe Phe Thr Arg His Gly Leu Asp Asp Arg Val Gly Val Leu Gly
 145 150 155 160
 Phe Asp Tyr Pro Ala Arg Thr Val Asn Val Tyr Phe Asn Asp Val Pro
 165 170 175
 Arg Glu Cys Phe Glu Pro Glu Thr Ile Arg Ser Thr Leu Arg Arg Thr
 180 185 190
 Gly Met Ala Glu Pro Ser Glu Gln Met Leu Arg Leu Gly Thr Gly Ala
 195 200 205
 Phe Gly Leu Tyr Val Thr Leu Gly Trp Asp Ser Pro Glu Ile Glu Arg
 210 215 220
 Ile Cys Tyr Ala Ala Ala Thr Thr Asp Leu Thr Thr Leu Pro Val Pro
 225 230 235 240
 Val Glu Pro Glu Ile Glu Lys Phe Val Lys Ser Val Pro Tyr Gly Gly
 245 250 255
 Gly Asp Arg Lys Phe Val Tyr Gly Val Ala Leu Thr Pro Lys Gly Glu
 260 265 270
 Tyr Tyr Lys Leu Glu Ser His Tyr Lys Trp Lys Pro Gly Ala Val Asn
 275 280 285
 Phe Ile
 290

<210> 23

<211> 873

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 23

| | |
|---|-----|
| gtggccgagc tctactcgac catcgaggaa tcggcccggc aactggaegt gccgtgttcg | 60 |
| cgcgaccggg tctggcccat cctgtccgcg tacggcgacg cgttcgccca tcccaggcgc | 120 |
| gtggtcgcct tccgggtggc gaccgcgctg cgtcacgcgg gcgagctgga ctgccggttc | 180 |
| cggacgcata cggacgaccg ggaccggtac gcctcgggcg tcgcccgggg cctcaccgcc | 240 |
| cgcacggacc acccgcgcg cgcgctgctc tccgaggtcc accggcgctg cccgggtggag | 300 |
| agccacggca tcgacttcgg ggtggtcggc ggcttcaaga agatctacgc ggccttcgcc | 360 |

ccggacgagc tgcaggtggc cacgtcgctc gccggcattc cggcgatgcc ccgcagcctc 420
 gccgcgaacg ccgacttctt caccgggcac ggctcgacg accgggtcgg cgtgctggga 480
 ttcgactacc cggcccggac cgtgaacgctc tacttcaacg acgtgccgcg tgagtgcctc 540
 gagccggaga ccatccggtc gacgctgcgc cggaccggga tggccgagcc gagcgagcag 600
 atgctccggc tcggcaccgg ggcgttcggg ctctacgtca cgctgggctg ggactccccg 660
 gagatcgagc ggatctgcta cgccgcggcg accacggacc tgaccacgct tccggtaccc 720
 gtggaaccgg agatcgagaa gtctgtgaaa agcgttcctg acggcggcgg ggaccggaag 780
 ttcgtctacg gcgtggcgct gacccccaaag ggggagtact acaaactcga gtcgcactac 840
 aaatggaagc cgggcgcggg gaacttcatt tga 873

<210> 24
 <211> 370
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 24

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Trp | Ala | Arg | Val | Lys | Asn | Trp | Val | Val | Ala | Leu | Ala | Val | Ala | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Val | Leu | Met | Ile | Ser | Ala | Leu | Ala | Gly | Asp | His | Pro | Ala | Pro | Glu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gly | Leu | Leu | Gly | Phe | Ala | Leu | Val | Ala | Ala | Ser | Gly | Leu | Ala | Leu |
| | | | 35 | | | | | 40 | | | | 45 | | | |
| Ala | Ala | Ser | Arg | Arg | Ala | Pro | Ile | Ala | Val | Leu | Val | Ala | Thr | Gly | Leu |
| | | | 50 | | | | 55 | | | | | 60 | | | |
| Cys | Val | Val | Gly | Tyr | Asn | Ala | Ile | Gly | Phe | Gly | Val | Pro | Ala | Ile | Ala |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Tyr | Leu | Phe | Ala | Val | Tyr | Ala | Ala | Val | Arg | Ala | Gly | His | Arg | Leu | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Leu | Gly | Ala | Ser | Ala | Ala | Leu | Leu | Val | Val | Leu | Pro | Leu | Ala | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Met | Val | Ser | Pro | Ala | Asp | Gly | Ala | Leu | Lys | Glu | Ala | Leu | Ala | Gln | Ser |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Arg | Gly | Val | Leu | Glu | Leu | Ala | Trp | Leu | Ile | Ala | Ala | Ala | Ala | Ala | Gly |
| | | | 130 | | | | 135 | | | | | 140 | | | |
| Glu | Ala | Leu | Arg | Gln | Ala | Glu | Arg | Arg | Ala | Asp | Glu | Ala | Glu | Arg | Thr |
| 145 | | | | 150 | | | | | | 155 | | | | 160 | |

Arg Glu Glu Thr Ala Arg Leu Arg Ala Thr Gln Glu Arg Leu His Ile
 165 170 175
 Ala Arg Glu Leu His Asp Ser Leu Thr His Gln Ile Ser Ile Ile Lys
 180 185 190
 Val Gln Ala Glu Val Ala Val His Leu Ala Arg Lys Arg Gly Glu Gln
 195 200 205
 Val Pro Glu Ser Leu Leu Ala Ile Gln Glu Ala Gly Arg Ala Ala Thr
 210 215 220
 Arg Glu Leu Arg Ala Thr Leu Glu Thr Leu Arg Asp Leu Thr Lys Ser
 225 230 235 240
 Pro Ser His Gly Leu Asp His Leu Pro Glu Leu Leu Ala Gly Ala Glu
 245 250 255
 Lys Ile Gly Leu Ala Thr Thr Leu Thr Ile Glu Gly Asp Gln Arg Asp
 260 265 270
 Val Pro Glu Ala Val Gly Arg Thr Ala Tyr Arg Ile Val Gln Glu Ser
 275 280 285
 Leu Thr Asn Thr Ala Arg His Ala Ser Ala Ala Ala Ala Val Arg
 290 295 300
 Ile Asp Tyr Arg Pro Asp Ala Leu Ser Ile Arg Ile Asp Asp Asp Gly
 305 310 315 320
 Thr Ala Arg Pro Gly Ala Ala Pro Val Pro Gly Val Gly Leu Leu Gly
 325 330 335
 Met His Glu Arg Val Leu Ala Leu Gly Gly Arg Leu Arg Ala Glu Pro
 340 345 350
 Arg Thr Gly Gly Gly Phe Thr Val Gln Ala Glu Leu Pro Val Val Arg
 355 360 365
 Val Pro
 370

<210> 25

<211> 1113

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 25

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|---|-----|
| gtgtgggccc gggatgaagaa ctgggtcgtc gcgttggtg tggcggcggt gctgatgatc | 60 |
| agcgcgctgg ccggtgacca tctgcccc gagggcctcg gtctgctcgg cttcgcgctg | 120 |
| gtggcggcga gcggcctggc gctggccgcc agtcgtcggg ccccgatcgc cgtgctggtc | 180 |
| gccaccgggc tgtgcgtggt gggctacaac gcgatcggct tcggggtgcc cgccatcgcg | 240 |
| tacctgttcg cgggtctacgc ggcgggtccgg gccgggcacc ggctcgtcac gctcggggcg | 300 |

agcgccgccc tgctcgctgt cctgccgctg gcgatcatgg tctcgcccgc ggacggcgcc 360
 ctcaaggagg cgctcgcgca gtcgcggggc gtgctggaac tggcctggct gatcgccgcg 420
 gcggcgggccg gtgaggcgct gcggcaggcc gaacggcgag cggacgaggc ggaacggacc 480
 cgcgaggaga ccgcccggct gcgcgccacc caggagcggc tgcacatcgc acgggagctg 540
 cactactcgc tcaccacca gatctcgatc atcaaggtgc aggcggaggt ggcggtccac 600
 ctggcccgcga agcggggcga gcaggtgccg gagtcgctgc tggcgatcca ggaggccggc 660
 cgggcggcga ctcgcgagct gcgcgcgacc ctggagacgc tgcgtgacct gaccaagtcc 720
 ccgtcgcacg ggctcgacca cctcccggag ctgctggccg gggccgagaa gatcggcctg 780
 gccaccacgc tgaccatcga gggcgaccag cgggacgtgc cggaggcggg gggccgcacc 840
 gcgtaccgga tcgtgcagga gtcgctcacc aacaccgccc ggcacgcctc cgccgcggcc 900
 gccgcggtcc ggatcgacta ccgcccggac gcgctgagca tccggatcga cgacgacggg 960
 acggcccggc cgggcgcccgc cccggtgccc ggcgtcgggc tgctggggat gcacgagcgc 1020
 gtctcgcgc tgggcggccg gctgcgggcg gaaccccgca ccggcggagg cttcaccgtc 1080
 caggccgaac tcccgggtgt gcgcgtccca tga 1113

<210> 26

<211> 220

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 26

Met Ile Arg Ile Met Leu Leu Asp Asp Gln Pro Leu Leu Arg Ser Gly
1 5 10 15

Phe Arg Ala Leu Leu Asp Ala Glu Asp Asp Ile Glu Val Val Ala Glu
20 25 30

Gly Gly Asn Gly Arg Glu Gly Leu Ala Leu Ala Arg Gln His Leu Pro
35 40 45

Asp Leu Ala Leu Ile Asp Ile Gln Met Pro Val Met Asp Gly Val Glu
50 55 60

Thr Thr Arg Gln Ile Val Ala Asp Pro Ala Leu Ala Gly Val Arg Val
65 70 75 80

Val Ile Leu Thr Asn Tyr Gly Leu Asp Glu Tyr Val Phe His Ala Leu
85 90 95

Arg Ala Gly Ala Thr Gly Phe Leu Val Lys Asp Ile Glu Pro Asp Asp
100 105 110

Leu Leu His Ala Val Arg Val Ala Ala Arg Gly Asp Ala Leu Leu Ala
 115 120 125
 Pro Ser Ile Thr Arg Met Leu Ile Asn Arg Tyr Val Ser Glu Pro Leu
 130 135 140
 Cys Ala Asp Val Thr Pro Gly Met Glu Glu Leu Thr Asn Arg Glu Arg
 145 150 155 160
 Glu Ala Val Ala Leu Ala Ala Arg Gly Leu Ser Asn Asp Glu Ile Ala
 165 170 175
 Asp Arg Met Val Ile Ser Pro Leu Thr Ala Lys Thr His Val Asn Arg
 180 185 190
 Ala Met Thr Lys Leu Gln Ala Arg Asp Arg Ala Gln Leu Val Val Phe
 195 200 205
 Ala Tyr Glu Ser Gly Leu Val Ser Pro Gly Asn Arg
 210 215 220

<210> 27
 <211> 663
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 27
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 ctcgacgccg aggacgacat cgaggtggtg gccgagggcg ggaacggccg ggagggcctg 120
 gcgctggccc ggcagcacct gcccgatctc gccctgatcg acatccagat gccggtcatg 180
 gacggcgctcg agacgacccg gcagatcgctc gcggatccgg cgctggcccg ggtacgcgtc 240
 gtcattctca ccaactacgg cctcgacgag tacgtcttcc acgcgctgcy gccggcgcc 300
 accggcttcc tgggtcaagga catcgagccg gacgacctgc tgcacgccgt gcgggtcgcc 360
 gcgcgcggtg acgcgctgct cgcgccgtcg atcaccgga tgctgatcaa caggtacgtg 420
 tcggagccgc tctgcgcgga cgtaacgccc ggcattggagg agctgaccaà ccgggaacgc 480
 gagggcggtcg ccttggccgc ccggggcctg tccaacgacg agatcgccga tcgcatggtg 540
 atcagcccgc tgaccgcgaa gacccacgtc aaccgcgcca tgaccaagct gcaggcccgc 600
 gaccgcgccc agctggtggt gttcgcttac gagtccggcc tgggtgcacc cggcaatcgc 660
 tga 663

<210> 28
 <211> 131
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 28

Met Phe Ile Arg Arg Leu Leu Thr Ala Ala Ala Ala Gly Val Leu Gly
1 5 10 15

Gly Leu Ala Leu Val Ala Pro Ala Ala Ala Gln Val Thr Ala Ala Asp
20 25 30

Gly Asp Gly Gly Ser Gly Arg Ala Gly Ser Val Leu Ala Leu Ala Leu
35 40 45

Ala Leu Leu Gly Leu Val Leu Gly Gly Trp Ala Leu Arg Ser Ala Gly
50 55 60

Arg Gly Gly Gly Arg Gly Asn Ala Ile Ala Ala Leu Val Leu Ala Val
65 70 75 80

Ala Gly Leu Ile Ala Gly Val Val Ala Leu Ala Gly Ser Asp Gly Gly
85 90 95

Val Gly Ser Gly Asn Gly Arg Gly Gly Ala Ile Val Ala Val Val Leu
100 105 110

Ala Leu Ile Gly Ile Ala Val Gly Gly Leu Ala Phe Thr Arg Ser Arg
115 120 125

Arg Ala Ala
130

<210> 29

<211> 396

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 29

atgttcatcc gtcgtttgct caccgccgcc gcagccggcg tcctcggtgg gctcgcactc 60

gtcgcaccgg cggccgcgca ggtgacggcc gccgacggtg acggtggttc cgcccgcgcc 120

ggatccgtgc tggecgtcgc gctcgcgttg ctccggcctcg tcctgggcgg gtgggcgttg 180

cgctccgcgg ggcgcggcgg cggtcgtggc aacgcgatcg ccgcgctggt gctcgcggtg 240

gccggcctga tcgccggcgt ggtcgccctg gccggctccg acggtggtgt cggcagcggc 300

aacggccgtg gtggcgccat cgtggccgtc gtgctggcgc tgatcgggat cgccgtcggc 360

ggcctggcat tcaccgctc ccggcgcgcc gcctga 396

<210> 30

<211> 154

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 30

Met Arg Lys Val Phe Ala Gly Leu Ala Ala Phe Leu Leu Leu Val Leu
1 5 10 15
Val Val Gln Phe Phe Leu Ala Ala Ser Gly Ala Phe Ser Asn Glu Ala
20 25 30
Asn Glu Glu Ala Phe Arg Pro His Arg Ile Leu Gly Leu Gly Ser Ile
35 40 45
Leu Val Ala Val Val Leu Thr Val Ala Ala Ala Val Met Arg Met Pro
50 55 60
Gly Arg Ile Ile Gly Leu Ser Gly Leu Val Ala Gly Leu Gly Ile Leu
65 70 75 80
Gln Ala Leu Ile Ala Val Ile Ala Lys Ala Phe Gly Asp Ser Ala Gly
85 90 95
Asp Ser Ala Val Gly Arg Tyr Val Phe Gly Leu His Ala Val Asn Gly
100 105 110
Leu Val Met Val Ala Val Ala Arg Val Ile Leu Arg Ser Val Arg Ala
115 120 125
Ala Pro Asp Thr Thr Thr Thr Pro Gly Val Asp Thr Thr Val Thr Gly
130 135 140
Pro Ala Ala Asp Ser Ala Arg Thr Ala Ser
145 150

<210> 31
<211> 465
<212> DNA
<213> Micromonospora sp. strain 046-EC011

<400> 31
atgcgcaaag tgttcgccgg actggcagcg ttctgtctgc tcgtgtctgt ggtgcagttc 60
ttctggccg ccagcggcgc gttcagcaac gaggccaacg aggaggcgtt ccgccctcac 120
cggatcctgg gcttggggag catcctcgtc gccgtggtgc tgacggtggc cgccgcggtg 180
atgcggatgc ccggccggat catcggcctg tccggcctgg tcgccgggct gggcatcctg 240
caggccctga tcgcggtcat cgccaaggcg ttcggcgact cggccggtga ctcggccgtc 300
ggccggtacg tgttcggcct gcacgcggtc aacggactgg tgatggtggc cgtcgcccgc 360
gtcatcctgc gcagcgtcg ggcggcgccg gacacgacca ccacgcccgg cgtggacacg 420
acggtcaccg gtccggcggc cgactcggcg cgaacggcgt catga 465

<210> 32
<211> 661
<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 32

Met Ser Thr Leu Gln Trp Ile Leu Val Asp His Val Val Ala Leu Leu
1 5 10 15
Gly Val Ala Thr Trp Phe Ala Thr Gly Val Thr Ala Ala Leu Gly Arg
20 25 30
His Arg Ile Ala Leu Ala Leu Leu Gly Ala Ala Val Leu Val Thr Val
35 40 45
Ala Arg Leu Gly Thr Val Ala Leu Leu Ala Asp Arg Gly Trp Trp Phe
50 55 60
Val Gln Glu Lys Val Leu Leu Gly Leu Pro Met Leu Gly Ala Ala Gly
65 70 75 80
Leu Val Ala Val Leu Leu Ala Gly Pro Arg Leu Leu Ala Ala Arg Gln
85 90 95
Ser Pro Ala Ala Asp Leu Pro Ala Gly Ala Leu Val Ala Val Leu Thr
100 105 110
Ala Gly Phe Ala Ala Leu Ala Gly Leu Val Val Thr Phe Thr Ala Gly
115 120 125
Tyr Pro Leu Thr Trp Ser Thr Ala Leu Ile Ala Val Ala Leu Val Cys
130 135 140
Ala Ala Ala Leu Leu Thr Ala Arg Val Val Gly Arg Pro Ala Ala Pro
145 150 155 160
Ala Ala Glu Ala Gly Ser Pro Glu His Thr Pro Ala Ala Ala Gly Pro
165 170 175
Thr Ala Leu Ser Arg Arg Arg Phe Leu Gly Val Ala Gly Gly Val Val
180 185 190
Ala Ala Gly Ala Gly Ala Thr Gly Val Gly Leu Leu Phe Arg Asp Pro
195 200 205
Glu Ala Met Val Thr Gly Gly Gly Pro Gly His Ala Gly Gly Ala Arg
210 215 220
Pro Lys Val Ser Val Ala Asp Leu Arg Gly Pro Gly Ala Pro Ala Ala
225 230 235 240
Gly Gly Thr Ala Arg Arg His Val Leu Thr Ala Arg Thr Gly Thr Val
245 250 255
Thr Ile Pro Ser Gly Arg Pro Ile Asp Ala Trp Ser Tyr Glu Gly Arg
260 265 270
Leu Pro Gly Pro Ala Ile Thr Ala Thr Glu Gly Asp Leu Ile Glu Val
275 280 285

Thr Leu Arg Asn Ala Asp Ile Glu Asp Gly Val Thr Val His Trp His
 290 295 300
 Gly Tyr Asp Val Pro Cys Gly Glu Asp Gly Ala Pro Gly Ala Thr Gln
 305 310 315 320
 His Ala Val Gln Pro Gly Gly Glu Phe Val Tyr Arg Phe Gln Ala Asp
 325 330 335
 Gln Val Gly Thr Tyr Trp Tyr His Thr His Gln Ala Ser His Pro Ala
 340 345 350
 Val Arg Lys Gly Leu Tyr Gly Thr Leu Val Val Thr Pro Arg Glu Asp
 355 360 365
 Arg Pro Glu Ala Glu Arg Gly Leu Asp Leu Thr Leu Pro Val His Thr
 370 375 380
 Phe Asp Asp Val Thr Ile Leu Gly Asp Gln Glu Gly Arg Ala Val His
 385 390 395 400
 Asp Val Arg Pro Gly Gln Pro Val Arg Leu Arg Leu Ile Asn Thr Asp
 405 410 415
 Ser Asn Pro His Trp Phe Ala Val Val Gly Ser Pro Phe Arg Val Val
 420 425 430
 Ala Val Asp Gly Arg Asp Leu Asn Gln Pro Gly Glu Val Arg Glu Val
 435 440 445
 Gly Leu Arg Leu Pro Ala Gly Gly Arg Tyr Asp Leu Thr Leu Ala Met
 450 455 460
 Pro Asp Ala Lys Val Thr Leu Leu Leu Asp Asn Asp Ser Asp Gln Gly
 465 470 475 480
 Val Leu Leu Arg Pro Pro Gly Val Gly Gly Gly Asp Arg Pro Leu Pro
 485 490 495
 Asp Thr Ala Asp Trp Pro Glu Phe Asp Leu Leu Gly Tyr Gly Glu Pro
 500 505 510
 Ala Pro Val Pro Phe Asp Ala Asp Asp Ala Asp Arg His Phe Thr Ile
 515 520 525
 Val Leu Asp Arg Ala Leu Ala Met Val Asp Gly Lys Pro Ala Tyr Ala
 530 535 540
 Gln Thr Val Asp Gly Arg Ala His Pro Ser Val Pro Asp Gln Leu Val
 545 550 555 560
 Arg Glu Gly Asp Val Val Arg Phe Thr Val Val Asn Arg Ser Leu Glu
 565 570 575
 Thr His Pro Trp His Leu His Gly His Pro Val Leu Ile Leu Ser Arg
 580 585 590

Asp Gly Arg Pro Tyr Ser Gly Ser Pro Leu Trp Met Asp Thr Phe Asp
 595 600 605
 Val Arg Pro Gly Glu Val Trp Glu Val Ala Phe Arg Ala Asp Asn Pro
 610 615 620
 Gly Val Trp Met Asn His Cys His Asn Leu Pro His Gln Glu Gln Gly
 625 630 635 640
 Met Met Leu Arg Leu Val Tyr Asp Gly Val Thr Thr Pro Phe Ala Ser
 645 650 655
 Thr Ser His Ala His
 660

<210> 33
 <211> 1986
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 33
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 tggttcgcaa cgggtgtcac ggcagctctc ggccgccacc ggatcgcggtt ggcgctcctc 120
 ggcgcgcggg tgctggtgac agtcgcccgc ctgggcaccg tggcgctgct ggccgaccgc 180
 ggctggtggt tcgtccagga gaaggttctg ctggggctgc cgatgctcgg cgccgcgggg 240
 ctcgctcgcg tgctcctggc cggcccgcgc ctgctcgcg cccggcagtc accggcgggc 300
 gacctgccgg cgggcgcgct ggtcgcggtg ctgaccgccg gcttcgccgc gctggccggc 360
 ctggtggtga cgttcaccgc cgggtacccg ctgacgtgga gcaccgcgct gatcgccgtc 420
 gccctcgtct gcgcgcgcgc gctgctcacc gcgcgggttg tcggacgacc cgccgccccg 480
 gccgcggagg cgggtcccc ggagcacacg ccggcgggcg cggggccac ggcgctgtcc 540
 cgccgcgggt tctcggcgt ggccggggga gtggtcgcgg cgggcgccgg cgccaccggc 600
 gtcggcctgc tcttcgcga cccggaggcg atggtcaccg gaggcggccc cggacacgcc 660
 ggtggcgccc gcccgaaggt ctccgtggcg gacctgcgcg gcccggcg cccggcgggc 720
 ggcggcacgg cgcgacgcca cgtgctcacc gcccggacgg gcaccgtcac gattccgtcc 780
 ggacgtccga tcgacgcctg gagctacgag ggccgcctgc ccgggccggc catcaccgcg 840
 accgagggcg acctgatga ggtgacgctc cgcaacgccg acatcgagga cggcgtcacc 900
 gtgcactggc acgggtacga cgtgccgtgc ggcgaggacg gcgcgccggg cgccacgcag 960
 cacgcggtgc agcccggcg cgagttcgtc taccggttcc aggcggacca ggtggggacg 1020
 tactggtacc acaccacca ggcgtcgcac cccgccgtgc gcaaagggct gtacgggacg 1080

ctcgtcgtga cgccgcgcga ggaccggccg gaagcggagc gcgggctgga cctgacgctg 1140
 ccggtgcaca cgttcgacga cgtcacgata ctcggcgacc aggagggacg cgccgtccac 1200
 gacgtccgcc cgggccagcc ggtgcgactg cgtctgatca acaccgactc caaccgcac 1260
 tggttcgccg tcgtcggtc gcccttcgc gtggtggccg tcgacggccg cgacctcaac 1320
 cagccgggcg aggtacgcga ggtcgggctc cgctgcccg ccggaggccg gtacgacctg 1380
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 gtctgtctgc gccgcgcggg cgtcggcggt ggtgaccgcc cgctgccgga caccgccgac 1500
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 gacgccgacc gccacttcac catcgtcctc gaccgggccc tggccatggt cgacggcaag 1620
 cccgcgtacg ccagaccgt cgacggtcgc gcacatccct ccgtccccga ccagctcgtc 1680
 cgggaggggg acgtcgtgcg cttcacggtg gtcaaccgga gcctcgaaac ccaccgtgg 1740
 cacctgcacg gccatccggt gctgatcctg tcccgcgacg gccggccgta ctccggcagc 1800
 ccgctgtgga tggacacctt cgacgtgcgg ccgggagagg tgtgggaggt ggcgttccgg 1860
 gcggacaatc cgggtgtctg gatgaaccac tgccacaacc tgccgcacca ggagcagggc 1920
 atgatgtgc ggctcgtcta cgacggtgtc accacgccct tcgccagcac gagccacgca 1980
 cactga 1986

<210> 34
 <211> 129
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 34

Met Thr Ala Asp Leu His Gly Leu Ala Ser Val Arg Tyr Ile Val Asp
 1 5 10 15

Asp Val Ser Ala Ala Ile Glu Phe Tyr Thr Thr His Leu Gly Phe Thr
 20 25 30

Val Ser Thr Ala Phe Pro Pro Ala Phe Ala Asp Val Val Arg Gly Pro
 35 40 45

Leu Arg Leu Leu Leu Ser Gly Pro Thr Ser Ser Gly Ala Arg Val Thr
 50 55 60

Pro Ala Asp Ala Ala Gly Cys Gly Arg Asn Arg Ile His Leu Ile Val
 65 70 75 80

Asp Asp Leu Asp Ala Glu Arg Glu Arg Leu Glu Arg Ala Gly Val Thr

Ser Val Val Leu Trp Ser Ile Gly Gly Ile Val Leu Ala Val Val Val
100 105 110

Ala Arg Arg Ala Arg Arg Pro Val Arg Ala Phe Val Ala Gly Thr Val
115 120 125

Ala Phe Thr Val Leu Ser Leu Ala Ala Pro Ala Phe Ala Arg Asp Thr
130 135 140

Pro Val Ser Thr Gln Leu Val Leu Ala Gly Thr His Val Ile Ala Gly
145 150 155 160

Ala Val Ile Ile Ser Ile Leu Ala Ala Arg Leu Ala Ala Pro Thr Pro
165 170 175

Pro Arg

<210> 37
<211> 537
<212> DNA
<213> Micromonospora sp. strain 046-EC011

<400> 37
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tcgccggcca ccgctccggt gtggctgggtc ggcgtgctgg ccaccctcgc cggggccgtg 180
gcccgggagg cggtcacgct cgccgcccgg ggcttcggcg taccgatgga ggcggccggc 240
gtctgggagg agcaggcgca ggcgatcccg gtgggggcca tcgccgcag cgctgtgctc 300
tggtcgatcg gcggaatcgt cctggcggtg gtcgtggcgc ggcgggcccg gcggcccgtg 360
cgtgccttcg tggccggcac cgtcgcgttc accgtgctgt ccctcgccgc gcccgcttc 420
gcccgggaca ccccggtgtc gacgcagctc gtctcgcgc gcacccacgt gatcgccggc 480
gccgtgatca tctccatcct ggccgcgcgg ctgcgcgcgc ccaccccgcc ccggtaa 537

<210> 38
<211> 661
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 38

Met Asp Gly Thr Glu Ser Asn Val Thr Gly Phe Pro Asp Leu Leu Ser
1 5 10 15

Gly Leu Gly Gly Asp Gly Arg Ala Phe Ala Leu Leu His Arg Pro Gly
20 25 30

Ala Ala Gly Cys Ala Tyr Val Glu Val Leu Thr Gly Glu Val Cys Asp

| 35 | 40 | 45 |
|--|----|----|
| Val Asp Thr Leu Gly Glu Leu Pro Leu Pro Thr Glu Pro Ala Thr Gly 50 55 60 | | |
| Ala Arg His Asp Leu Leu Val Ala Val Pro Tyr Arg Gln Val Thr Glu 65 70 75 80 | | |
| Arg Gly Phe Asp Cys His Asp Asp Gly Ala Pro Leu Leu Ala Met Arg 85 90 95 | | |
| Val His Glu Gln Phe Gly Leu Asp Arg Gly Gln Ala Leu Ala Gly Leu 100 105 110 | | |
| Pro Glu Arg Gly Val Pro Val Thr Asp Ala Asp Phe Asp Leu Ser Asp 115 120 125 | | |
| Glu Asp Tyr Ala Ala Ile Val Lys Arg Val Val Gly Asp Glu Ile Gly 130 135 140 | | |
| Leu Gly Ala Gly Ser Asn Phe Val Ile Arg Arg Thr Phe Thr Ala Arg 145 150 155 160 | | |
| Leu Ala Asp Tyr Ser Ile Ala Thr Glu Leu Ala Leu Phe Arg Arg Leu 165 170 175 | | |
| Leu Thr Gly Glu Leu Gly Ser Tyr Trp Thr Phe Leu Phe His Ser Gly 180 185 190 | | |
| Ala Gly Thr Phe Ile Gly Ala Ser Pro Glu Arg His Val Ser Met Ile 195 200 205 | | |
| Asp Gly Thr Val Ser Met Asn Pro Ile Ser Gly Thr Tyr Arg His Pro 210 215 220 | | |
| Pro Asn Gly Pro Ala Val Ser Gly Leu Leu Glu Phe Leu Asn Asp Pro 225 230 235 240 | | |
| Lys Glu Ala Asn Glu Leu Tyr Met Val Val Asp Glu Glu Leu Lys Met 245 250 255 | | |
| Met Ala Arg Met Cys Ala Ser Gly Gly Gln Val His Gly Pro Phe Leu 260 265 270 | | |
| Lys Glu Met Ala Arg Val Thr His Ser Glu Tyr Ile Leu Thr Gly Arg 275 280 285 | | |
| Ser Asp Leu Asp Val Arg Asp Val Leu Arg Glu Thr Leu Leu Ala Pro 290 295 300 | | |
| Thr Val Thr Gly Ser Pro Ile Glu Asn Ala Phe Arg Val Ile Thr Arg 305 310 315 320 | | |
| His Glu Thr Thr Gly Arg Gly Tyr Tyr Gly Gly Val Leu Ala Leu Met 325 330 335 | | |
| Gly Arg Asp Ser Ala Gly Ser Arg Thr Leu Asp Ser Ala Ile Met Ile | | |

| | | |
|---|-----|-----|
| 340 | 345 | 350 |
| Arg Thr Ala Glu Ile Asp Asp Ala Gly Thr Leu Arg Leu Gly Val Gly | | |
| 355 | 360 | 365 |
| Ala Thr Leu Val Arg Asp Ser Lys Pro Glu Ser Glu Val Ala Glu Thr | | |
| 370 | 375 | 380 |
| Arg Ala Lys Ala Gly Ala Met Arg Ala Ala Leu Gly Leu Gly Val Asp | | |
| 385 | 390 | 395 |
| Pro Asp Gly Pro Asp Gly Gly Arg Thr Thr Ala Ala Arg Ala Arg Ser | | |
| | 405 | 410 |
| Ser Leu Ala Thr Asp Pro Arg Val Arg Arg Ala Leu Arg Glu Arg Asn | | |
| | 420 | 425 |
| Thr Thr Leu Ser Arg Phe Trp Leu Asp Gly Ala Glu Arg Arg Thr Pro | | |
| | 435 | 440 |
| Asn Pro Ala Leu Thr Gly Arg Arg Val Leu Val Val Asp Asn Glu Asp | | |
| | 450 | 455 |
| Thr Phe Met Ala Met Leu Asp His Gln Leu Arg Ala Leu Gly Leu Arg | | |
| 465 | 470 | 475 |
| Ser Ser Ile Ala Arg Phe Asp Ser Arg Leu Arg Pro Asp Gly His Asp | | |
| | 485 | 490 |
| Leu Val Val Val Gly Pro Gly Pro Gly Asp Pro Gly Asp Leu Thr Asp | | |
| | 500 | 505 |
| Pro Arg Met Arg Thr Leu Arg Gly Leu Thr Arg Asp Leu Leu Ala Gly | | |
| | 515 | 520 |
| Thr Val Pro Phe Leu Ser Ile Cys Leu Gly His Gln Val Leu Ala Ala | | |
| | 530 | 535 |
| Glu Leu Gly Phe Pro Leu Ala Arg Arg Ala Val Pro Asn Gln Gly Val | | |
| 545 | 550 | 555 |
| Gln Lys Arg Ile Asp Leu Phe Gly Arg Pro Glu Leu Val Gly Phe Tyr | | |
| | 565 | 570 |
| Asn Thr Tyr Thr Ala Arg Ser Ala His Asp Val Val Ala Gly Gly Arg | | |
| | 580 | 585 |
| Arg Gly Pro Ile Glu Ile Ser Arg Ser Pro Asp Ser Gly Asp Val His | | |
| | 595 | 600 |
| Ala Leu Arg Gly Pro Gly Phe Arg Ser Val Gln Phe His Leu Glu Ser | | |
| | 610 | 615 |
| Val Leu Thr Gln His Gly Pro Arg Ile Leu Gly Asp Leu Leu Val Ser | | |
| 625 | 630 | 635 |
| Leu Leu Ala Asp Gly Thr Ala Ala Ala Ala Ala Glu Ala Ala Gly Arg | | |

645

650

655

Arg Gly Asn Arg Pro
660

<210> 39

<211> 1986

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 39

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| gacggggcgcg ccttcgcctt gctgcaccgg cccggcgcgg ccgggtgcgc gtacgtggag | 120 |
| gttctgaccg gcgaggtgtg cgacgtggac actctcggcg agctgcccct gccaccgag | 180 |
| ccggcgaccg gcgcgcgga cgacctgctc gtggcggtgc cgtaccggca ggtcaccgaa | 240 |
| cggggggttcg actgccacga cgacggcgcg ccgctgctcg cgatgcgcgt ccacgagcag | 300 |
| ttcgggctcg accgcggaca ggcgctggcg ggcctgcccg aacgcggtgt gccggtgacc | 360 |
| gacgccgact tcgacctcag cgacgaggac tacgccgcga tcgtcaagcg ggtggtgggt | 420 |
| gacgagatcg ggctggggcg cggatccaac ttctgcatcc ggcgcacctt caccgcgcgg | 480 |
| ctggccgact actcgatcgc caccggaactg gcgctcttcc gccggttgct gaccggcgaa | 540 |
| ctgggttctt actggacgtt tctgttccac tccggcgccg gcacgttcat cggcgcgta | 600 |
| ccggaacgac acgtcagcat gatcgacgga accgtctcga tgaatcccat cagcgggacc | 660 |
| taccggcacc ccccgaacgg cccggccggt tccggtctgc tggaattcct gaacgacccg | 720 |
| aaagaggcta acgaactcta catggtcgtc gacgaggaac tgaaaatgat ggcgcggatg | 780 |
| tgcgctcccg gcggccaggt gcacggcccc ttctcaagg aaatggcgcg ggtgacgcac | 840 |
| tccgagtaca tctgaccgg ccgcagcgac ctggacgtgc gcgacgtgct gcgggagacc | 900 |
| ctgctcgcgc cgacggtcac cggcagcccc atcgagaacg cgttccgggt catcaccgc | 960 |
| cacgagacga ccggcccgcg ctactacggc ggcgtgctcg cgttgatggg ccgtgactcg | 1020 |
| gccggcagcc gtacgtcga ctcggccatc atgatccgca ccgccgagat cgacgacgcg | 1080 |
| ggcacgctgc gcctgggctg cggcgccacc ctctgcggg actccaagcc ggagtcggag | 1140 |
| gtggccgaga cgcgggccaa ggcgggcgac atgcgcgcgg cgctcggcct cggcgtcgac | 1200 |
| ccggacggcc cggacggcg gcggaccacg gccgcgcggg ctcttcgtc cctggccacc | 1260 |
| gacccccggg tacggcgggc gttgcgcgag cgcaacacca cactgtcgag gttctggctc | 1320 |
| gacggcgcgg agcggcgcac cccgaacccg gcgctgaccg gacgcgcgt gctcgtcgtc | 1380 |

gacaacgagg acacgttcat ggccatgctc gaccaccagt tgcggggccct cgggctgcgg 1440
tcgagcatcg cccgggttga cagccggctg cggccggacg gacacgacct cgtcgtcgtc 1500
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cacctggagt ccgtctcac ccagcacggc ccacggatcc tgggcgacct gctgggtctcc 1920
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ccgtga 1986

<210> 40
<211> 427
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 40

Val Lys Thr Thr Val Asp Val Leu Val Gln Lys Tyr Gly Gly Thr Ser
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Leu Gln Thr Leu Asp Arg Val Arg His Ala Ala Leu Arg Ile Ala Glu
20 25 30
Ala Arg Arg His Gly Ser Ala Val Thr Val Val Val Ser Ala Arg Gly
35 40 45
Ser Arg Thr Asp Asp Leu Leu Arg Leu Ala Ala Asp Val Gly Ala Ala
50 55 60
Gly Pro Ser Arg Glu Leu Asp Gln Leu Leu Ala Val Gly Glu Ser Glu
65 70 75 80
Ser Ala Ala Leu Met Ala Leu Ala Leu Thr Gly Leu Gly Val Pro Ala
85 90 95
Val Ser Leu Thr Gly His Gln Ala Glu Ile His Thr Thr Asp Arg His
100 105 110
Gly Asp Ala Leu Ile Ser Arg Ile Gly Ala Ala Arg Val Glu Ala Ala
115 120 125
Leu Gly Arg Gly Glu Val Ala Val Val Thr Gly Phe Gln Gly Ile Asp
130 135 140

Arg Ala Gly Asp Val Ala Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr
 145 150 155 160
 Ala Val Ala Leu Ala Ala Arg Leu Arg Ala Ser Ala Cys Glu Ile Tyr
 165 170 175
 Thr Asp Val Asp Gly Val Phe Ser Ala Asp Pro Arg Ile Leu Pro Ala
 180 185 190
 Ala Arg Cys Leu Pro Trp Val Glu Pro Gly Val Met Ala Glu Met Ala
 195 200 205
 Phe Ala Gly Ala Arg Val Leu His Thr Arg Cys Ile Glu Leu Ala Ala
 210 215 220
 Met Glu Gly Val Glu Val Arg Val Arg Asn Ala Ser Ser Gln Ala Pro
 225 230 235 240
 Gly Thr Ile Val Val Asp Arg Pro Asp Asp Arg Pro Leu Glu Thr Arg
 245 250 255
 Arg Ala Val Val Ala Val Thr His Asp Thr Asp Val Val Arg Val Leu
 260 265 270
 Val His Cys Arg Asp Gly Arg Arg Asp Met Ala Pro Asp Val Phe Glu
 275 280 285
 Val Leu Ala Ala His Gly Ala Val Ala Asp Leu Val Ala Arg Ser Gly
 290 295 300
 Pro Tyr Glu Ser Glu Phe Arg Met Gly Phe Thr Ile Arg Arg Ser Gln
 305 310 315 320
 Ala Glu Ala Val Arg Thr Ala Leu His Asp Leu Thr Ala Ser Phe Asp
 325 330 335
 Gly Gly Val His Phe Asp Glu Asn Val Gly Lys Val Ser Val Val Gly
 340 345 350
 Met Gly Leu Leu Ser Arg Pro Glu His Thr Ala Arg Leu Met Ala Ala
 355 360 365
 Leu Ala Ala Ala Gly Ile Ser Thr Ser Trp Ile Ser Thr Ser Gln Met
 370 375 380
 Arg Leu Ser Val Ile Val Ser Arg Asp Arg Thr Val Asp Ala Val Glu
 385 390 395 400
 Ala Leu His Arg Ala Phe Arg Leu Asp Arg Ser Glu Pro Ala Asp Ala
 405 410 415
 Thr Ser Leu Thr Ser Arg Arg Ser Ala Thr Ala
 420 425

<210> 41
 <211> 1284
 <212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 41

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acagtggtcg tgtcggcgcg cggcagccgg accgacgacc tgctgcggct ggcggccgac      180
gtcggcgccg cgggtccgtc ccgggaactc gaccagttgc tcgcagtcgg cgagtccgag      240
tcggcggcgc tgatggcgct ggcgttgacc gggctgggag tgccggccgt ctcgctgacc      300
gggcaccagg cggagatcca caccaccgac cggcacggcg acgcgctgat ctcgcggatc      360
ggggcggcgc ggggtggaagc ggcgctgggc cgtggcgagg tcgccgtggt caccggattc      420
cagggcatcg accgggccgg tgacgtcgcc acgctggggc gcggcggctc cgacacgaca      480
gcggtggcgc tcgcggcccg gctccgcgcg tcggcgtgcg agatctacac cgacgtggac      540
ggcgtcttca gcgccgacc ccgcatactt ccggcggcgc gttgcctgcc gtgggtggag      600
cccggcgta tgccggagat ggcgttcgcc ggcgcgcggg tcctgcacac ccgatgcac      660
gagctggccg ccatggaagg ggtcgaagtg cgcgtgcgca acgcgtcgtc gcaggcgccc      720
ggaacgatag tcgtggaccg gcccgacgac cggccgctgg agaccggcg ggccgtggtg      780
gcggtcacc accgacacga tgcgtccgc gtgctggtgc actgccgcga cggccgccgg      840
gacatggcac ccgacgtgtt cgaggtgctg gccgcccatg gggcggtggc ggacctggtg      900
gcccggtccg ggcctacga gagcgagttc cggatggggg tcaccatccg ccgcagccag      960
gccgaagcgg tcgggaccgc gctgcacgac ctcaccgct ccttcgacgg cgggggtccac     1020
ttcgacgaga acgtcggcaa ggtgtccgtg gtcggcatgg gcctgctcag ccgccccgag     1080
cacacggccc ggctgatggc ggcgctggcc gggcggggga tctcgacgag ctggatctcc     1140
acctcccaga tcgggtgtc ggtgatcgtg tcgcgggacc gcaccgtcga cgccgtcgaa     1200
gccctgcacc gcgcgttcgg cctggaccgg tccgagccgg cggacgccac gtccctgacc     1260
tcccgccgtt ccgccaccgc ctga                                           1284
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<210> 42

<211> 274

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 42

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Leu Phe Arg Arg Gly Asp Gly Arg Leu Leu Val Val Pro Leu Asp His
 20 25 30
 Ser Val Thr Asp Gly Pro Leu Arg Arg Gly Asp Leu Asn Ser Leu Leu
 35 40 45
 Gly Glu Leu Ala Gly Thr Gly Val Asp Ala Val Val Leu His Lys Gly
 50 55 60
 Ser Leu Arg His Val Asp His Gly Trp Phe Gly Asp Met Ser Leu Ile
 65 70 75 80
 Val His Leu Ser Val Ser Thr Arg His Ala Pro Asp Pro Asp Ala Lys
 85 90 95
 Tyr Leu Val Ala His Val Glu Glu Ala Leu Arg Leu Gly Ala Asp Ala
 100 105 110
 Val Ser Val His Val Asn Leu Gly Ser Pro Gln Glu Ala Arg Gln Ile
 115 120 125
 Ala Asp Leu Ala Ala Val Ala Gly Glu Cys Asp Arg Trp Asn Val Pro
 130 135 140
 Leu Leu Ala Met Val Tyr Ala Arg Gly Pro Gln Ile Thr Asp Ser Arg
 145 150 155 160
 Ala Pro Glu Leu Val Ala His Ala Ala Thr Leu Ala Ala Asp Leu Gly
 165 170 175
 Ala Asp Ile Val Lys Thr Asp Tyr Val Gly Thr Pro Glu Gln Met Ala
 180 185 190
 Glu Val Val Arg Gly Cys Pro Ile Pro Leu Ile Val Ala Gly Gly Pro
 195 200 205
 Arg Ser Ala Asp Thr Pro Thr Val Leu Ala Tyr Val Ser Asp Ala Leu
 210 215 220
 Arg Gly Gly Val Ala Gly Met Ala Met Gly Arg Asn Val Phe Gln Ala
 225 230 235 240
 Glu Gln Pro Gly Leu Met Ala Ala Ala Val Ala Arg Leu Val His Glu
 245 250 255
 Pro Arg His Val Pro Asp Arg Tyr Asp Val Asp Asp Arg Leu Ala Leu
 260 265 270

Thr Ser

<210> 43
 <211> 825
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 43
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 cgcggcgacc tgaactcgct gctcgggtgag ctgcgccggca ccggcgtgga cgccgtggtg 180
 ctgcacaagg gcagcctgcg gcacgtcgac cacggctggt tcggcgacat gtcgctgac 240
 gtgcatctga gcgtgagcac ccggcacgcc ccggacccgg acgcgaagta cctggctcgcg 300
 cacgtggagg aggcgctgcg gctggggcgcc gacgcgggtca gcgtgcacgt caacctcggc 360
 tcaccgcagg aggcgcggca gatcgccgac ctggcggcgg tggcggggga gtgcgaccgc 420
 tggaacgtcc cgctgctggc catggtgtac gcccgcgggc cgcagatcac cgactcccgg 480
 gcaccggagc tgggtggcgca cgccgcgacg ctgcgccggg acctcggcgc cgacatcgtc 540
 aagaccgact acgtgggcac gcccgagcag atggccgagg tgggtgcgcgg ctgcccgatc 600
 ccgctgatcg tggccggcgg cccgcgctcg gccgacactc cgacggtgct cgcctacgtc 660
 tcggacgcgc tgcgcggcgg cgtggccggg atggccatgg gccgcaacgt gttccaggcc 720
 gagcagcccg gcctgatggc cgccgcgctg gcacggctgg tgcacgagcc acggcacgtg 780
 ccggaccggt acgacgtcga cgaccggctc gcccttaagt cctga 825

<210> 44
 <211> 367
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 44

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Leu | Cys | Trp | Leu | Asp | Ile | Arg | Asn | Val | Asn | Gly | Ala | Lys | Glu |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Ala | Ile | Val | Glu | Glu | Ala | Val | His | Gln | Arg | Val | Asp | Ala | Val | Val | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Asp | Pro | Ala | Asp | Leu | Glu | Thr | Leu | Pro | Pro | Thr | Val | Lys | Lys | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Phe | Pro | Gln | Gly | Gly | Pro | Leu | Pro | Glu | Lys | Leu | Glu | Pro | Ala | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Val | Ile | Val | Glu | Pro | Ala | Arg | His | Gly | Glu | Pro | Ala | Glu | Leu | Ala |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ala | Arg | Tyr | Pro | Glu | Val | Glu | Phe | Gly | Arg | Phe | Val | Glu | Ile | Val | Asp |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Ala | Asp | Ser | Leu | Glu | Asp | Ala | Cys | Arg | Ser | Ala | Arg | His | Asp | Arg | Trp |
| | | 100 | | | | | | 105 | | | | | | 110 | |

Ser Leu Leu Tyr Phe Arg Asp Pro Thr Lys Ile Pro Leu Glu Ile Val
 115 120 125

Leu Ala Ala Ala Ala Gly Ala Glu Gly Ser Ile Ile Thr Gln Val Ala
 130 135 140

Asp Val Glu Glu Ala Glu Ile Val Phe Gly Val Leu Glu His Gly Ser
 145 150 155 160

Asp Gly Val Met Leu Ala Pro Arg Ala Val Gly Glu Ala Thr Glu Leu
 165 170 175

Arg Thr Ala Ala Val Ser Thr Ala Ala Asp Leu Ser Leu Val Glu Leu
 180 185 190

Glu Val Thr Gly Ile Arg Arg Val Gly Met Gly Glu Arg Ala Cys Val
 195 200 205

Asp Thr Cys Thr Asn Phe Arg Leu Asp Glu Gly Ile Leu Val Gly Ser
 210 215 220

His Ser Thr Gly Met Ile Leu Cys Cys Ser Glu Thr His Pro Leu Pro
 225 230 235 240

Tyr Met Pro Thr Arg Pro Phe Arg Val Asn Ala Gly Ala Leu His Ser
 245 250 255

Tyr Thr Leu Ser Ala Gly Gly Arg Thr Asn Tyr Leu Ser Glu Leu Val
 260 265 270

Ser Gly Gly Arg Val Leu Ala Val Asp Ser Gln Gly Lys Ser Arg Val
 275 280 285

Val Thr Val Gly Arg Val Lys Ile Glu Thr Arg Pro Leu Leu Ala Ile
 290 295 300

Asp Ala Val Ser Pro Ser Gly Thr Arg Val Asn Leu Ile Val Gln Asp
 305 310 315 320

Asp Trp His Val Arg Val Leu Gly Pro Gly Gly Thr Val Leu Asn Val
 325 330 335

Thr Glu Leu Thr Ala Gly Thr Lys Val Leu Gly Tyr Leu Pro Val Glu
 340 345 350

Lys Arg His Val Gly Tyr Pro Ile Asp Glu Phe Cys Ile Glu Lys
 355 360 365

<210> 45

<211> 1104

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 45

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60

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 cttcccccca cggatgaagaa ggtgctgttc ccgcagggcg ggccgctgcc ggagaagctg 180
 gaaccggccg acctggtgat cgtcgagccg gcccggcacg gcgagcccg cgagctggcg 240
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 acccaggtcg ccgacgtcga ggaggcggag atcgtcttcg gcgtcctgga gcacggctcg 480
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 ctgctggcga tcgacgcggg cccccctcc gggacacgcg tcaacctcat cgtccaggac 960
 gactggcacg tgccgctgct cgggcgggc ggcaccgtgc tcaacgtgac cgagctgacc 1020
 gccggcacga aggtgctcgg ttacctgccg gtggagaagc ggcacgtcgg ctacccgac 1080
 gacgagttct gcacgagaa gtga 1104

<210> 46
 <211> 253
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 46

Met Thr Ala Gln Pro Val Leu Asp Phe His Val Arg Leu Ala Pro Arg
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Pro Gly Ala Arg Glu Arg Leu Leu Ala Ala Leu Arg Glu Cys Gly Leu
 20 25 30

Ala Arg Ala Val Val Cys Ala Gly Gly Thr Ile Asp Leu Asp Arg Leu
 35 40 45

Ser Arg Gln Leu Val Thr Gly Gly His Val Glu Thr Asp Ala Asp Asn
 50 55 60

Asp Ala Val Ala Ala Ala Cys Ala Gly Thr Asp Gly Arg Leu Val Pro

| | | | |
|---|-----|-----|-----|
| 65 | 70 | 75 | 80 |
| Phe Phe Phe Ala Asn Pro His Arg Pro Ala Glu Ala Tyr Arg Ala Arg | 85 | 90 | 95 |
| Ala Ala Glu Phe Arg Gly Leu Glu Ile Ser Pro Ala Val His Gly Val | 100 | 105 | 110 |
| Ala Leu Thr Asp Pro Arg Val Ala Asp Leu Val Ala Val Ala Ala Glu | 115 | 120 | 125 |
| Phe Asp His Pro Val Tyr Val Val Cys Leu Asp Arg Pro Gly Ala Gly | 130 | 135 | 140 |
| Val Ala Asp Leu Val Gly Leu Ser Arg Arg Phe Pro Gln Val Ser Phe | 145 | 150 | 155 |
| Val Leu Gly His Ser Gly Val Gly Asn Ile Asp Leu Tyr Ala Leu Thr | 165 | 170 | 175 |
| Leu Ile Gln Asp Glu Pro Asn Ile Ser Leu Glu Thr Ser Gly Gly Tyr | 180 | 185 | 190 |
| Thr Cys Val Ala Glu Ala Ala Leu Arg Arg Leu Gly Asp Asp Arg Val | 195 | 200 | 205 |
| Val Phe Gly Ser Glu Tyr Pro Leu Gln His Pro Ala Val Glu Leu Ala | 210 | 215 | 220 |
| Lys Phe Gln Ala Leu Arg Leu Pro Pro Glu Arg Trp Arg Arg Ile Ala | 225 | 230 | 235 |
| Trp Asp Asn Ala His Arg Leu Leu Gly Glu Glu Lys Arg | 245 | 250 | |

<210> 47
 <211> 762
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 47
 atgaccgcgc agccggtgct ggacttccac gtacgcctgg cgccccggcc cggggcgcg 60
 gagcggctgc tcgccgcgct gcgcgagtg gggctggcgc gggcgggtggt gtgcgcgggc 120
 ggcaccatcg acctggaccg gctgtccgc cagctcgtca ccggcggcca cgtcgagacc 180
 gacgccgaca acgacgcggt ggcgggcgcc tcgccggca ccgacggccg gctggtgccg 240
 ttctttcttcg ccaaccgcga ccggccggcc gaggcgtacc gggccgcgc cgccgagttc 300
 cgcggcctgg agatctcacc cgccgtccac ggcgtcgccc tgaccgaccc gcggtcgcc 360
 gacctcgtgg ccgtggcggc ggagttcgac catccggtgt acgtggtctg cctggaccga 420
 cccggcgcg gcggtggcca cctggtcggc ctgagccgcc ggttcccga ggtgagcttc 480

Arg Ala Leu Phe Val Gly Gly Glu Pro Met Thr Asp Ala Arg Arg Arg
 210 215 220
 Arg Ile Ser Arg Leu Trp Gly Val Pro Val Ile Glu Glu Tyr Gly Ser
 225 230 235 240
 Thr Glu Thr Gly Ser Leu Ala Gly Glu Cys Pro Glu Gly Arg Leu His
 245 250 255
 Leu Trp Ala Asp Arg Ala Leu Phe Glu Val Tyr Asp Pro Asp Thr Gly
 260 265 270
 Ala Val Arg Ala Asp Gly Asp Gly Gln Leu Val Val Thr Pro Leu Phe
 275 280 285
 Arg Glu Ala Met Pro Leu Leu Arg Tyr Asn Leu Glu Asp Asn Val Ser
 290 295 300
 Val Ser Tyr Asp Asp Cys Gly Cys Gly Trp Lys Leu Pro Thr Val Arg
 305 310 315 320
 Val Leu Gly Arg Ser Ala Phe Gly Tyr Arg Val Gly Gly Thr Thr Ile
 325 330 335
 Thr Gln His Gln Leu Glu Glu Leu Val Phe Ser Leu Pro Glu Ala His
 340 345 350
 Arg Val Met Phe Trp Arg Ala Lys Ala Glu Pro Ala Leu Leu Arg Val
 355 360 365
 Glu Ile Glu Val Ala Ala Ala His Arg Val Ala Ala Glu Ala Glu Leu
 370 375 380
 Thr Ala Ala Ile Arg Ala Ala Phe Gly Val Asp Ser Glu Val Thr Gly
 385 390 395 400
 Leu Ala Pro Gly Thr Leu Ile Pro Leu Asp Ala Leu Thr Ser Met Pro
 405 410 415
 Asp Val Val Lys Pro Arg Ser Leu Phe Gly Pro Asp Glu Asp Trp Ser
 420 425 430
 Lys Ala Leu Leu Tyr Tyr
 435

<210> 49

<211> 1317

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 49

gtgagcgagc caagttcgag cctgccccgg ctcggccagt ggcacggcct cgaggacctg 60

cggcgccctcc aggagaagca actggcggag acgttcacct gggcgggccg gtcgccgttc 120

taccggggcg ggctggcctc cggcgcgccg ccggtgacgc ccgccgacct ggccgacctg 180

ccgctgacca ccaagcagga cctgcgggac aactaccctc tcggcatgct cgccgtgccc 240
 cggaacggc tggcgaccta ccacgagtcg agcgggaccg ccgggaagcc caccctcc 300
 tactacaccg cggaggactg gaccgacctg gcggagcgct tcgcccgcaa gtggatcggc 360
 atgtccgccc acgacgtctt cctgggtccgc acgccgtacg cgctgctgct gaccgggcat 420
 ctgccccacg ccgcagcccg gctgcgtggg gccacgggtg tacctggcga caaccggtcg 480
 ctggcgatgc cgtacgcccg ggtgggtccg gtgatgcacg acctggacgt cacgctcacc 540
 tggtcggtgc cgacggagtg cctgatctgg gccgcccgcg cgatcgcggc cgggcaccgg 600
 cccgacatcg acttcccggc gctgcgcgcg ctgttcgctg gcggcgagcc gatgaccgac 660
 gcccgccggc ggccgatcag ccgcctgtgg ggggtgccgg tcatcgagga gtacggctcg 720
 acggagaccg gcagcctggc cggggagtgcc cccgagggac gcctgcacct gtgggcccgc 780
 cgggcgctgt tcgaggtgta cgaccgggac accggcgccg tccgcgcgga cggcgacggc 840
 cagctcgtgg tcacgccgct gttccgggag gcgatgccgc tgctgcggta caacctggag 900
 gacaacgtgt cgggtctcta cgacgactgc ggatgcggct ggaagctgcc caccgtgcgg 960
 gtgctcggcc ggtcggcggt cggctaccgg gtcggcggca ccaccatcac ccagcaccag 1020
 ctggaggaac tgggtcttct cctgccggag gcgcaccggg tgatgttctg gcgggccaag 1080
 gcggagccgg cgctgttgcg ggtcgagatc gaggtggccg ccgcgcaccg ggtcgcgcc 1140
 gaggcggagc tgaccgccgc gatccgggcc gccttcggcg tggacagcga ggtcaccggc 1200
 ctggcgccgg gaacctgat cccgctcgac gcgctgacca gcatgccgga cgtggtgaag 1260
 ccacgcagcc tggtcgggtc ggacgaggac tggagcaaag cgctcctcta ctactga 1317

<210> 50

<211> 396

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 50

Met Pro Gln Met Arg Val Ala Val Ala Gly Ala Gly Ile Ala Gly Leu
1 5 10 15

Ala Phe Ala Ala Ala Leu Arg Arg Thr Gly Ile Asp Cys His Val Tyr
20 25 30

Glu Gln Ala Asp Gln Leu Met Glu Val Gly Ala Gly Val Gln Val Ala
35 40 45

Pro Asn Ala Thr Arg Leu Leu His Arg Leu Gly Leu Arg Asp Arg Leu
50 55 60

Arg Thr Val Ala Val Ala Pro Gln Ala Ile Glu Met Arg Arg Trp Asp
 65 70 75 80
 Asp Gly Thr Leu Leu Gln Arg Thr Gln Leu Gly Ser Val Cys Gly Arg
 85 90 95
 Arg Phe Gly Ala Pro Tyr Tyr Val Val His Arg Ala Asp Leu His Ser
 100 105 110
 Ser Leu Leu Ser Leu Val Pro Pro Asp Arg Val His Leu Gly Ala Arg
 115 120 125
 Leu Thr Ala Val Thr Gln Thr Ala Asp Glu Ala Tyr Leu His Leu Ser
 130 135 140
 Asn Gly Thr Thr Val Ala Ala Asp Leu Val Val Gly Ala Asp Gly Ile
 145 150 155 160
 His Ser Val Ala Arg Glu Gln Ile Val Ala Asp Arg Pro Arg Phe Ser
 165 170 175
 Gly Gln Ser Ile Tyr Arg Gly Leu Val Pro Ala Glu Arg Val Pro Phe
 180 185 190
 Leu Leu Thr Glu Pro Arg Val Gln Leu Trp Phe Gly Pro Asp Gln His
 195 200 205
 Cys Val Cys Tyr Pro Val Ser Ala Gly Arg Gln Val Ser Phe Gly Ala
 210 215 220
 Thr Val Pro Ala Thr Asp Trp Arg Gln Glu Ser Trp Ser Gly Arg Gly
 225 230 235 240
 Asp Val Thr Gln Leu Ala Ala Ala Tyr Ala Gly Trp His Pro Asp Val
 245 250 255
 Thr Arg Leu Ile Ala Ala Ala Asp Arg Val Gly Arg Trp Ala Leu His
 260 265 270
 Asp Arg Asp Ser Ile Asp Arg Leu Ser Ala Gly Arg Val Thr Leu Ile
 275 280 285
 Gly Asp Ala Ala His Pro Met Leu Pro Phe Gln Ala Gln Gly Ala Asn
 290 295 300
 Gln Ala Val Glu Asp Ala Val Val Leu Ala Val Cys Leu Ala Gly Val
 305 310 315 320
 Glu Pro Ala Gly Leu Gly Ala Ala Leu Arg Arg Tyr Glu Arg Ile Arg
 325 330 335
 Leu Pro Arg Thr Thr Arg Ile Gln Arg Gln Ser Arg Ala Asn Ala Glu
 340 345 350
 Met Phe His Leu Ala Asp Gly Ala Asp Gln Arg Arg Arg Asp Val Ala
 355 360 365

Ala Gln Ser Ser Ser Gly Leu Asp Arg His Glu Trp Leu Phe Gly Tyr
 370 375 380

Asp Ala Glu Lys Ala Thr Thr Thr Ser Gly Ser Ala
 385 390 395

<210> 51
 <211> 1191
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 51
 atgccgcaga tgaggggtcgc cgtggccggc gccggcatcg ccgggctcgc cttcgccgcc 60
 gccctgcgcc ggaccgggat cgactgccac gtgtacgaac aggccgacca gtcctatggag 120
 gtgggcgcgg gcgtgcaggt cgcgccgaac gccaccggc tgctgcaccg gctgggcctg 180
 cgtgaccgcc tgcgtacggt ggctgtcgcg ccgcaggcga tcgagatgcg ccgctgggac 240
 gacggcacgc tgctgcaacg caccagctg ggcagcgtgt gcggacgccg cttcggcgcg 300
 ccgtactacg tgggtgcaccg cgcggacctg cacagcagcc tgctgtcgtt ggtgccgccg 360
 gaccgggtgc acctggggcg ccgcctcacc gccgtgacgc agaccgccga cgaggcgtac 420
 ctgcacctgt ccaacggcac cacggtcgcg gcggatctcg tcgtgggcgc cgacggcatc 480
 cactcggctc cgcgggagca gatcgtggcg gaccggccgc gcttctccgg acagtccatc 540
 taccgcgggc tgggtgccggc cgagcgggtg ccgttctcgc tcaccgaacc ccgggtgcag 600
 ttgtgggttc ggccggacca gcaactgcgtc tgctaccggg tgtccgccgg ccggcaggtg 660
 agcttcggcg cgacgggtgcc cgccaccgac tggcggcagg agtcgtggtc gggccggggc 720
 gacgtgacgc aactcgcggc cgcgtacgcg ggctggcacc cggacgtcac ccggctgac 780
 gccgcggccg accgggtcgg cagggtggcg ctgcacgacc gggacagcat cgaccggctc 840
 agcgcgggac ggggtgacct gatcggcgac gccgcgcacc cgatgctgcc gttccaggcg 900
 cagggcgcg accaggccgt cgaggacgcg gtgggtgctc cggctctgct ggccggcgtg 960
 gaaccggcg ggctgggcgc cgcgtgcgc cgctacgaac ggatccgcct gcccgggacc 1020
 acccggtacc agcggcagtc ccgggccaac gccgagatgt tccacctggc cgacggcgcc 1080
 gaccagcgcc gccgggacgt cgccgcacaa tcctcgtccg gcctggaccg ccacgaatgg 1140
 ctcttcgggt acgacgccga gaaagccacc acgaccagcg ggagcgctg a 1191

<210> 52
 <211> 261
 <212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 52

Met Glu Leu Thr Gly Ile Glu Ser Lys Val Ala Leu Val Thr Gly Ala
1 5 10 15
Gly Gln Gly Ile Gly Ala Ala Val Ala Gly Val Leu Ala Arg Ala Gly
20 25 30
Ala Gln Val Ala Ala Val Asp Arg Asn Ala Glu Ala Leu Thr Thr Val
35 40 45
Val Thr Lys Leu Ala Ala Glu Gly Asp Ser Ala Arg Ala Tyr Cys Val
50 55 60
Asp Val Cys Asp Ser Glu Ala Val Asp Ala Leu Val Arg Arg Val Glu
65 70 75 80
Asp Glu Met Gly Pro Val Ala Ile Leu Val Asn Ala Ala Gly Val Leu
85 90 95
His Thr Gly Arg Val Val Glu Leu Ser Asp Arg Gln Trp Arg Arg Thr
100 105 110
Phe Ser Val Asn Ala Asp Gly Val Phe His Val Ser Arg Ala Val Ala
115 120 125
Arg Arg Met Val Gly Arg Arg Arg Gly Ala Ile Val Thr Val Ala Ser
130 135 140
Asn Ala Ala Gly Val Pro Arg Thr Glu Met Ala Ala Tyr Ala Ala Ser
145 150 155 160
Lys Ala Ala Ser Ala Gln Phe Thr Arg Cys Leu Gly Leu Glu Leu Ser
165 170 175
Gly Tyr Gly Ile Arg Cys Asn Val Val Ser Pro Gly Ser Thr Asp Thr
180 185 190
Pro Met Leu Arg Ala Met Leu Gly Glu Gly Ala Asp Pro Ser Ala Val
195 200 205
Ile Glu Gly Thr Pro Gly Ala Tyr Arg Val Gly Ile Pro Leu Arg Lys
210 215 220
Leu Ala Gln Pro Arg Asp Val Ala Glu Ala Val Ala Tyr Leu Val Ser
225 230 235 240
Asp Gln Ala Gly His Val Thr Met His Asp Leu Tyr Val Asp Gly Gly
245 250 255
Ala Ala Leu His Val
260

<210> 53

<211> 786

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 53

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ggcgccgccc tggccggtgt cctggcgagg gcgggcgcgc aggtggcggc ggtggaccgc   120
aacgccgagg cgctgaccac cgctcgtgacg aagctcgccg ccgagggcga ctcggcgcgc   180
gcctactgcg tcgacgtgtg cgacagcgag gcggtggacg cgctggtgcg ccgggtcgag   240
gacgagatgg ggccggtcgc catcctggtc aacgccgccg gcgtgctgca caccggacgg   300
gtcgtcgagc tgtcggaccg gcagtggcgc cggaccttct cggtgaacgc cgacggcgtg   360
ttccacgtgt cccgggcggg ggcgcggcgg atggtgggcc gccgtcgtgg cgcgatcgtc   420
accgtggcgt cgaacgccgc cggggtgccg cgtaccgaga tggccgcgta cgccgcctcc   480
aaggccgcgt ccgcgcagtt caccgcgtgc ctggggcttg agctgtccgg ctacggcatc   540
cggtgcaacg tgggtctgcc cggctccacc gacaccccca tgctgcgggc catgctcggc   600
gagggcgccc acccgagcgc ggtgatcgag ggcacgccgg gcgcgtaccg cgtcggcatc   660
ccgctgcgca agctggccca gccgcgcgac gtggccgagg cggtcgccta tctggtgtcc   720
gaccaggcgg gccacgtgac catgcacgac ctgtacgtcg acggcggcgc ggccctgcac   780
gtgtga                                           786
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<210> 54

<211> 224

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 54

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Met Ala Met Thr Pro Ile Ala Pro Tyr Arg Met Pro Gly Asp Gly Asp
1           5           10          15
Leu Pro Gly Thr Ala Leu Pro Trp Arg Pro His Pro Asp Arg Ala Ala
20          25          30
Val Leu Val His Asp Leu Gln Arg Tyr Phe Leu Arg Pro Phe Glu Ala
35          40          45
Gly Glu Ser Pro Met Ala Glu Leu Leu Pro Asn Val Ala Lys Leu Leu
50          55          60
Ala Thr Ala Arg Ala Ala Gly Val Pro Val Leu Tyr Thr Ala Gln Pro
65          70          75          80
Gly Gly Met Ser Arg Gln Asp Arg Gly Leu Leu His Asp Leu Trp Gly
85          90          95
```

Pro Gly Met Ser Ser Ala Glu Asp Asp Arg Gly Ile Val Asp Asp Val
100 105 110

Ala Pro Gln Pro Gly Asp Thr Val Leu Thr Lys Trp Arg Tyr Ser Ala
115 120 125

Phe Phe Arg Ser Asp Leu Glu Glu Arg Leu Arg Gly Ala Gly Arg Asp
130 135 140

Gln Leu Val Val Cys Gly Val Tyr Ala His Met Gly Cys Leu Ile Thr
145 150 155 160

Ala Cys Asp Ala Phe Ser Arg Asp Ile Glu Ala Phe Leu Val Ala Asp
165 170 175

Ala Leu Ala Asp Leu Ser Arg Glu Asp His Leu Met Ala Leu Arg Tyr
180 185 190

Ala Ala Asp Arg Cys Ala Val Pro Leu Trp Thr Ala Asp Val Leu Asp
195 200 205

Gly Leu Ala Asp Ala Ala Gly Arg Pro Asp Gln Ser Ser Thr Gln Arg
210 215 220

<210> 55

<211> 675

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 55

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tacttctctgc gcccgttcga ggccgggggag tccccgatgg ccgaactgct ccccaacgtc 180

gcgaagctgc tcgccacggc gcggggcggcc ggcggtgccgg tgctgtacac cgcgacagccc 240

ggcggcatga gccggcagga ccgcggggtg ctgcacgacc tgtggggccc cgccatgagc 300

agcgccgagg acgaccgggg catcgtcgac gacgtcgccc cgcagccggg cgacacggtg 360

ctgaccaagt ggcgctacag cgcgttcttc cgcagcgacc tggaggagcg actgcgcggt 420

gcgggacggg accagctcgt ggtctgcggc gtgtacgcgc acatgggggtg cctgatcacc 480

gcctgcgacg cgttcagccg cgacatcgag gcgttctctgg tggcggacgc gctggccgac 540

ctatcgcgcg aggaccacct gatggcgctg cgctacgccg cggaccgctg cgcggtgccg 600

ttgtggacgg cggatgtgct ggacgggctg gcggacgccg ccggggcgtcc ggatcagagc 660

agcacccaac gatga 675

<210> 56

<211> 233.
 <212> PRT
 <213> Micromonospora sp. strain 046-ECO11

<400> 56

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Met Ser Asp Arg Thr Arg Val Val Val Val Gly Gly Thr Ser Gly Ile
1           5           10           15

Gly Arg His Phe Ala Arg Phe Cys Ala Glu Arg Gly Asp Asp Val Val
          20           25           30

Ile Thr Gly Arg Ser Ala Ala Arg Thr Lys Thr Val Ala Asp Glu Ile
      35           40           45

Gly Gly Arg Thr Arg Gly Leu Ala Leu Asp Leu Ala Glu Pro Glu Thr
      50           55           60

Ile Ala Asp Ala Leu Ala Asp Val Pro His Val Asp Arg Leu Val Val
65           70           75           80

Ala Ala Leu Asp Arg Asp Tyr Asn Thr Val Arg Ala Tyr Arg Pro Gly
          85           90           95

Asp Ala Ala Arg Leu Leu Thr Val Lys Leu Val Gly Tyr Thr Ala Val
      100           105           110

Leu His Ala Leu Ala Pro Arg Met Thr Asp Glu Ser Ala Val Val Leu
      115           120           125

Leu Gly Gly Leu Ala Ser His Arg Pro Tyr Pro Gly Ser Thr Ser Val
      130           135           140

Thr Thr Ala Asn Gly Gly Ile Ser Ala Leu Val Arg Thr Leu Ala Val
145           150           155           160

Glu Leu Ser Pro Val Arg Val Asn Ala Leu His Pro Ser Ile Val Ser
      165           170           175

Asp Thr Pro Phe Trp Ser Asp Lys Pro Ala Ala Arg Glu Ala Ala Ala
      180           185           190

Thr Arg Ala Leu Ser Arg Arg Pro Val Thr Met Gln Asp Cys Ala Glu
      195           200           205

Ala Ile Asp Phe Leu Leu Thr Asn Arg Ser Ile Asn Gly Val Asn Leu
      210           215           220

Asn Ile Asp Gly Gly Asp Val Leu Ile
225           230

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<210> 57
 <211> 702
 <212> DNA
 <213> Micromonospora sp. strain 046-ECO11

<400> 57

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 gcccgattct ggcgcgaacg cggagacgac gtggtgatca ccggccgttc ggcgccccgg 120
 accaagaccg tggcggacga gatcggcggg cggacccgtg ggctcgtctt cgacctggcc 180
 gagccggaga cgatcgcgga cgcgctcgcc gacgtgccgc acgtcgaccg gctcgtggtc 240
 gcggcgctgg accgcgacta caacaccgtc cgcgcgtacc ggccggggcga cgcggcgcg 300
 ctgctgaccg tcaagctggt cggctacacg gcggtcctgc acgccctcgc cccgcggatg 360
 accgacgaga ggcagtcgt gctgctcggc ggcctggcca gccaccggcc gtatccccggc 420
 tccacctccg tcacgaccgc caacggcggg atcagcgcgc tggtgccggac cctggctgtg 480
 gaactctcgc cgggtccgggt caacgccctg caccgagca tcgtctccga caccgccgttc 540
 tggagcgaca agcccgccgc gcgggaggcc gccgcgaccc gcgcgctcag ccgacggccg 600
 gtcaccatgc aggactgcgc cgaggcgatc gacttcctgc tgacgaaccg ctcgataaac 660
 ggggtcaacc tgaacatcga cggcggggac gtgctcatct ga 702

<210> 58

<211> 246

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 58

Met Thr Ser Ala Leu Arg Thr Ser Ala Trp Thr Tyr Asp Asp Phe Thr
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Ser Arg Glu Leu Asp Pro Ala Arg Trp Ala Ile Met Ser Ile Ala Gly
20 25 30

Ala Asp Gly Gln Thr His Arg Tyr Gln Asp Arg Asn Ala Gln Val Arg
35 40 45

Thr Gly Asp Gly Arg Leu Glu Leu Thr Val Asp Pro Phe Thr Arg Phe
50 55 60

His Asp Thr Asp Pro Arg Gln Asn Asn Ala Lys Gln Met Tyr Arg Ser
65 70 75 80

Val Arg Arg Phe Ala Val Pro Ala Glu Gly Ser Leu Thr Val Glu Val
85 90 95

Glu Met Gly Val Arg Thr Tyr Arg Gln Ile Pro His Asp Leu Leu Asp
100 105 110

Ala Phe Gly Thr Val Asn Leu Phe Asp Leu Glu Thr Gly Val Val Phe
115 120 125

Asn Ala Ala Ala Thr Asn Asp Thr Val Tyr Ala Thr Val Glu Arg Leu

130

135

140

Val Leu Pro Gly Val Thr Gln Pro His Glu His Tyr Ile His Arg Val
145 150 155 160

Val Leu Asp Val Pro Thr Glu Pro Gly Arg Ala His Gly Tyr Ala Ile
165 170 175

Thr Tyr Arg Ala Pro Thr Ser Glu Val Glu Phe His Val Asp Gly Arg
180 185 190

Leu Ala Tyr Trp Ala Arg Val Pro Val Pro Val Thr Gly Phe His Ala
195 200 205

Gly Met Ala Leu Phe Ser Ala Arg Asp Leu Ala Arg Tyr Pro Arg Glu
210 215 220

Gln Arg Glu His Gly Gln Gly Ala Thr Gly Trp Trp Gly Pro Trp Arg
225 230 235 240

Ile Ala Ser Gly Val Arg
245

<210> 59

<211> 741

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 59

atgacgtcgg cactgagaac cagcgcgtgg acgtacgacg acttcaccag ccgcgagctg 60
gaccccgccc gctgggcgat catgtcgatc gccggcgcgg acgggcagac ccacaggtac 120
caggaccgca acgcccaggt ccgcaccggc gacgggcggc tggagctgac cgtcgacccg 180
ttcaccgct tccacgacac cgatccccgg cagaacaacg ccaagcagat gtaccggctg 240
gtgcggcgct tgcgctgcc ggcgaggggc tcgctgaccg tcgaggtgga gatgggctg 300
cggacgtacc ggcagatccc gcacgacctg ctggacgctg tcggcacggt gaacctgttc 360
gacctggaga ccggcgctcg gttcaacgcc gccgccacga acgacaccgt gtacgcgacg 420
gtcgagcgcc tgggtgctgcc cggcgtgacc cagccgcacg agcactacat ccaccgggtg 480
gtcctggacg tgccgacgga gccgggcccgg gcgcacggat acgccatcac ctaccgggcg 540
ccgacgtcgg aggtggagtt ccacgtcgac ggccggctcg cctactgggc gcgggtcccc 600
gtgccggtga ccggattcca cgccggcatg gcgctcttct ccgcccgga cctggccccg 660
tacccccgag agcagcgagg gcacgggcag ggcgcgaccg ggtggtgggg gccgtggcgg 720
atcgctccg gcgtcagatg a 741

<210> 60

<211> 111
 <212> PRT
 <213> Micromonospora sp. strain 046-ECO11

<400> 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Ala | Ala | Pro | Ala | Thr | Asp | Gly | Gly | Arg | Tyr | Leu | Ala | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| His | His | Ser | Ala | Glu | Phe | Arg | Glu | Leu | Arg | Arg | Arg | Ser | Ser | Thr | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Leu | Trp | Ala | Ser | Val | Ala | Phe | Phe | Gly | Trp | Trp | Phe | Leu | Gly | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Ala | Thr | Tyr | Ala | Pro | Asp | Phe | Phe | Arg | Glu | Lys | Val | Ala | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Val | Asn | Val | Gly | Leu | Leu | Phe | Val | Phe | Leu | Ser | Phe | Ala | Phe | Val |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Thr | Leu | Ala | Ala | Phe | Tyr | Leu | Arg | Tyr | Ala | Arg | Thr | His | Leu | Asp |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Pro | Leu | Ser | Glu | Lys | Ile | Arg | Ala | Asp | Leu | Glu | Gly | Ala | Ser | Arg | |
| | | | 100 | | | | | 105 | | | | | 110 | | |

<210> 61
 <211> 336
 <212> DNA
 <213> Micromonospora sp. strain 046-ECO11

<400> 61

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| atggacacgg | cagctccggc | aacggacggc | ggtcgctacc | tcgccgtcca | tcacagcgca | 60 |
| gagttcaggg | aactacggcg | acgatcgagc | acgttcacgc | tctgggccag | cgtcgccttc | 120 |
| ttcggctggt | ggttcctcgg | cagcctgctc | gccacctacg | cgccggactt | cttcggggag | 180 |
| aaggtggccg | gcccgggtcaa | cgtgggtctg | ctcttcgtct | tcctgtcggt | cgccttcgtg | 240 |
| gtgacgctcg | ccgccttcta | cctgcgttac | gcccgcacgc | atctcgatcc | gctcagcgag | 300 |
| aagatccgtg | ccgacctgga | aggagcgccc | cgatga | | | 336 |

<210> 62
 <211> 559
 <212> PRT
 <213> Micromonospora sp. strain 046-ECO11

<400> 62

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Ile | Leu | Ala | Asp | Pro | Pro | Pro | Pro | Val | Asp | Asn | Thr | Trp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Thr | Pro | Ala | Ile | Ala | Val | Pro | Val | Thr | Ile | Val | Leu | Ala | Leu | Ala |

| 20 | | | | | 25 | | | | | 30 | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Val | Leu | Tyr | Leu | Val | Arg | Ser | Ala | Arg | Ala | Ser | Thr | Thr | Thr | Ala | Asp | | | | |
| 35 | | | | | 40 | | | | | 45 | | | | | | | | | |
| Gly | Phe | Leu | Leu | Ala | Asp | Arg | Arg | Ile | Gly | Pro | Val | Gln | Asn | Ala | Leu | | | | |
| 50 | | | | | 55 | | | | | 60 | | | | | | | | | |
| Ala | Val | Ala | Ser | Ala | Pro | Leu | Met | Tyr | Ser | Thr | Met | Tyr | Ile | Ile | Thr | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| Gly | His | Ile | Ala | Leu | Ser | Gly | Tyr | Asp | Ala | Ile | Leu | Leu | Met | Thr | Ala | | | | |
| 85 | | | | | 90 | | | | | 95 | | | | | | | | | |
| Phe | Thr | Met | Gly | Thr | Met | Leu | Ala | Leu | Phe | Leu | Phe | Ala | Gly | Pro | Val | | | | |
| 100 | | | | | 105 | | | | | 110 | | | | | | | | | |
| Arg | Asn | Val | Gly | Gly | Tyr | Thr | Leu | Gly | Asp | Leu | Leu | Ala | Val | Arg | Thr | | | | |
| 115 | | | | | 120 | | | | | 125 | | | | | | | | | |
| Arg | Glu | Arg | Pro | Ala | Arg | Ile | Ala | Ser | Ala | Val | Leu | Thr | Leu | Leu | Thr | | | | |
| 130 | | | | | 135 | | | | | 140 | | | | | | | | | |
| Tyr | Val | Met | Leu | Thr | Val | Ile | Met | Met | Ala | Ala | Ile | Ala | Phe | Ile | Phe | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | |
| Asn | Arg | Trp | Phe | Gly | Val | Asp | Ala | Leu | Val | Gly | Leu | Val | Leu | Pro | Val | | | | |
| 165 | | | | | 170 | | | | | 175 | | | | | | | | | |
| Phe | Val | Val | Gly | Leu | Ile | Thr | Val | Gly | Tyr | Val | Tyr | Leu | Gly | Gly | Met | | | | |
| 180 | | | | | 185 | | | | | 190 | | | | | | | | | |
| Leu | Gly | Val | Thr | Arg | Ile | Leu | Val | Phe | Lys | Leu | Val | Leu | Ser | Val | Val | | | | |
| 195 | | | | | 200 | | | | | 205 | | | | | | | | | |
| Val | Val | Gly | Val | Leu | Thr | Ala | Trp | Val | Leu | Ala | Arg | Phe | Asp | Leu | Asn | | | | |
| 210 | | | | | 215 | | | | | 220 | | | | | | | | | |
| Leu | Phe | Ser | Leu | Leu | Glu | Arg | Ala | Glu | Ala | Asn | Ala | Ala | Pro | Val | Pro | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | |
| Ser | Gly | Ser | Asp | Leu | Leu | Gly | Pro | Gly | Arg | Leu | Phe | Gly | Glu | Gly | Ala | | | | |
| 245 | | | | | 250 | | | | | 255 | | | | | | | | | |
| Thr | Thr | Leu | Val | His | Leu | Ser | Lys | Leu | Phe | Ala | Ile | Ala | Val | Gly | Val | | | | |
| 260 | | | | | 265 | | | | | 270 | | | | | | | | | |
| Ala | Ala | Ile | Pro | Phe | Leu | Phe | Met | Arg | Asn | Phe | Ala | Val | Thr | Ser | Gly | | | | |
| 275 | | | | | 280 | | | | | 285 | | | | | | | | | |
| Arg | Asp | Ala | Arg | Arg | Ser | Thr | Gly | Trp | Ala | Ser | Met | Ile | Ile | Val | Gly | | | | |
| 290 | | | | | 295 | | | | | 300 | | | | | | | | | |
| Phe | Tyr | Leu | Cys | Leu | Ser | Val | Val | Gly | Leu | Gly | Ala | Val | Ala | Ile | Leu | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | |
| Gly | Arg | Asp | Asn | Ile | Gly | Val | Ile | Lys | Ala | His | Arg | Asp | Ile | Ser | Phe | | | | |

| 325 | 330 | 335 |
|---|-----------------------------|-----|
| Pro Lys Leu Ala Asp Glu Leu Gly Gly | Pro Val Met Val Gly Ser Leu | |
| 340 | 345 | 350 |
| Ala Gly Val Ala Val Leu Thr Ile Val Gly Val Phe Ala Pro Leu Leu | | |
| 355 | 360 | 365 |
| His Ser Ala Val Thr Thr Val Thr Lys Asp Leu Asn Val Ile Arg Gly | | |
| 370 | 375 | 380 |
| Arg Arg Leu Asp Pro Ala Ala Glu Leu Arg Asp Ile Lys Arg Asn Thr | | |
| 385 | 390 | 395 |
| Leu Ile Ile Gly Val Gly Ser Val Leu Leu Ala Val Val Met Leu Pro | | |
| 405 | 410 | 415 |
| Val Arg Thr His Ile Phe Ile Pro Thr Ser Ile Asp Ile Ala Gly Ala | | |
| 420 | 425 | 430 |
| Val Val Leu Pro Ile Val Val Tyr Ala Leu Phe Trp Arg Arg Phe Asn | | |
| 435 | 440 | 445 |
| Thr Arg Gly Leu Gln Trp Thr Val Tyr Gly Gly Leu Ala Leu Thr Ala | | |
| 450 | 455 | 460 |
| Phe Leu Val Leu Phe Ser Asn Gly Val Ser Gly Glu Pro Asp Ala Ile | | |
| 465 | 470 | 475 |
| Phe Pro Asp Arg Asn Phe Lys Phe Val Asp Val Glu Pro Ala Leu Ile | | |
| 485 | 490 | 495 |
| Thr Val Pro Val Gly Phe Leu Leu Gly Tyr Leu Gly Ser Ile Thr Ser | | |
| 500 | 505 | 510 |
| Arg Glu Arg Asp Asp Ala Ala Phe Ala Glu Met Gln Val Arg Ser Leu | | |
| 515 | 520 | 525 |
| Thr Gly Ala Val Val Thr Gly Pro Pro Arg Pro Ala Ala Val Asp Asp | | |
| 530 | 535 | 540 |
| Glu Asp Arg Asp Gly Arg Gln Asp Arg Ala Pro Ser Pro Val Ser | | |
| 545 | 550 | 555 |

<210> 63

<211> 1680

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 63

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cgcgccagca ccaccaccgc ggacggcttc ctgctggccg accggcggat cgggcccgtg 180

cagaacgcgc tggcgggtggc ctccgcgccg ctgatgtact cgacgatgta catcatcacc 240

| | |
|--|------|
| ggccacatcg cgctcagcgg ctacgacgcc atcctgctga tgaccgcctt caccatgggc | 300 |
| accatgctcg cgctgttcct cttcgccggg cgggtgcgca acgtgggcgg ctacacgctc | 360 |
| ggtgacctgc tcgcggtccg taccggggag cggccggcgc ggatcgcgtc ggcggtgctc | 420 |
| acgctgctga cgtacgtcat gctgacgggtg atcatgatgg ccgccatcgc gttcatcttc | 480 |
| aaccgctggt tcggcgctga cgccctcgtc ggctgggtcc tcccggtgtt cgtcgctggt | 540 |
| ctgatcacgg tgggggtacgt gtacctcggc gggatgctcg gggtcacccg catcctggtg | 600 |
| ttcaagctgg tgctgtcggt ggtcgctgtg ggcgtgctga ccgcctgggt gctggccccgc | 660 |
| ttcgacctga acctcttcag cctgctggag cggggccgagg cgaacgcggc gccggtgccc | 720 |
| agcggcagcg acctgctggg cccggggcgg ctgttcggcg agggcgcgac cacgctcggtg | 780 |
| cacctgtcga agctgttcgc catcgccgtc ggagtggcgg ccattccgtt cctgttcattg | 840 |
| cgcaacttcg cggtgaccag cggggcgggac gcgcgccggt cgaccgggtg ggcgtcgatg | 900 |
| atcatcgctg ggttctacct gtgcctgtcc gtcgtcgggc tcggtgccgt cgcgatcctc | 960 |
| ggccgggaca acatcggcgt catcaaggcc caccgcgaca tcagcttccc caagctcgcc | 1020 |
| gacgagctcg gcggtccggt gatggtcggc tccttgccg gcgtcgcggt cctgacgac | 1080 |
| gtcggcgctc tcgcgccgct gctgcacagc gccgtgacga cggtgaccaa ggacctgaac | 1140 |
| gtgatccgcg gccggcggtt ggatccggcc gccgagctgc gggacatcaa gcgcaacacc | 1200 |
| ctgatcatcg gcgtcggtc cgtgctgctg gcggtcgtga tgctgccggt acggacccac | 1260 |
| atcttcatcc cgacctgat cgacattgcc ggcgcgggtg tcctgccgat cgtcgtctac | 1320 |
| gcgttggttct ggcgggcgtt caacaccgc ggactgcagt ggacggtcta cggcggcctc | 1380 |
| gcgctcaccg cgttctcggt gctgttctcc aacggtgtct cgggcgagcc ggacgccatc | 1440 |
| ttcccgacc gcaacttcaa gtctgtggac gtcgagcccg cgctgatcac ggtgccggtc | 1500 |
| ggcttcctgc tcggctacct cggtcgtac accagccggg agcgcgacga cgccgcgttc | 1560 |
| gccgagatgc aggtccggtc cctcacggga gctgtcgtca cgggaccgcc gcggccggcc | 1620 |
| gccgtggacg acgaggaccg cgacggccgc caggaccggg cgcccagccc ggtgagctga | 1680 |

<210> 64

<211> 5960

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 64

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|---|----|

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|--|------|
| ggtcggcatg gtcaccgcgc tggcgctcgc ccgtaacggc gtcgcctgcg tctcgtcga | 120 |
| ccagggcttc gagacgtcgg tccatcccaa gctggactac gtcaacgccc gcagcatgga | 180 |
| gttctctcgc cagttcggcc tcgccgacga cgtccgtgcc gccggcgteg cgcgcgagca | 240 |
| ccggggccgac gtcattctggt cgaccggcct ggccgggtgag ccgatcacca ggtggggggt | 300 |
| gccctcgggtg acgcaggagt ggccgcgcgt cgcgcgagcac aacgacggca cccagccggc | 360 |
| cgagccccggc cagcggatct cccagatcga cctggaaccg gtcttgccggg cccgctgccg | 420 |
| gcgggagccc cttgtcgacc tgcgcctcgg cgtacggttc gactcgtga cccaggacga | 480 |
| cgccgggggtc accagcgctc tcgccgacga caccggcggc gaggtccggg tgcggtcgga | 540 |
| gtacgtggtc ggggtgcgacg gcgcgtcgag ccaggctcgc cgggcccgtg gcacgtgga | 600 |
| ggaggggttc gacgtgcccg gcctgccggg cgccttcatt gtgcacttca ccagccggga | 660 |
| cctggacagc ctgcaccggc acggccgggt ctggcactac ttcgcgttcc ggtacgtgat | 720 |
| catcgcccag gacgaggtcg acacctggac cgcgcacgtc aacggcgteg acccgaacga | 780 |
| gttcgacgag ccgccggccg acccggaggc gttcctgctc gacacgatcc gcaccgagct | 840 |
| gcggatcgac aaggtgctgc tcacctcgcg ctggcgctcc ggcttcattg tcgccgacag | 900 |
| gtaccgcgcc ggccgggtgc tgctcgccgg tgactcggcc caccggatgt tccccaccgg | 960 |
| cgcgtacggc atgaacaccg gcacggcgga cgcgcgtcgc gtggcctgga agctggccgc | 1020 |
| tgctcgtccg ggcttcggcg gccccgggct gctcgacagc tacgacgccg aacgccgccc | 1080 |
| ggtggggcgcg cgcaacatgc gcacctcgca ccggcacctg ggcgtgcacc tgcggggcg | 1140 |
| cgagctcctg cgcggcgggc ccccgctgcc gtccgtcgcg gccttcctcg acgccgagcg | 1200 |
| ggcgagaaac gaggaccggg ggatcgagct cggctaccgc tactccgggt cgcgggtgct | 1260 |
| ctggccggag ggccccgggg agccctcgga cgaccgcggg gcgtacgcc cgacgacctg | 1320 |
| gcccggcgcc cgtccgccc gctcctgct gagcgacggg cagcagatct tcgaccggtt | 1380 |
| cgaccgcgcc tcgttcaccc tcgtggactt caccggtgac ggccgcgccg gtccgctgct | 1440 |
| ggcgggcgcg gccgcgcggg ggctcccggc caccacacc gtggtgaccg acccccgggc | 1500 |
| tcgtgagctg tgggaacgcg acctcgctct gctgcggccg gaccaccacg tcgcctggcg | 1560 |
| gggaaacacc gtgccgcggg accccgacgc cgtgggtccag cgcgtgcggg gtggcgata | 1620 |
| ggcgcgacgt gccgtcaccg gcggccccgg tcacgcgcac acgcgaccgg ccggtccggc | 1680 |
| tgactctcga ctggaggaca gatgcagcaa tccggttcaa cggcggaacg cagcccactc | 1740 |

| | |
|---|------|
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| gcggagacct gtcaggcggt ggcgtcggcc ccgccgctgg tcccacccgg ggaggtacgg | 1860 |
| gggttcgggc agctgttgtc ggagctggcg tcgaccgacg ggctcctgct gcagttgggc | 1920 |
| gactgcgccg agagcctcta cgagtgcacc ccccggcaca cctcggacaa gatcgaggtc | 1980 |
| atcgaccggc tgggggaccg gctcagcgag ctcaccgggc gcaacgtgct gcgggtgggc | 2040 |
| cggtatggccg ggcagttcgc caagccccgg tcgcaggcga cggagtggca cgacgcgctg | 2100 |
| agcatccctt ccttcgcgg ccacatgac aattccgagc tggccgcgcc cggtagcgcc | 2160 |
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| ctgcgcgcc accgggagg caaccggcgt gccgcgcga ccgaggggcc gtggtcgagc | 2280 |
| cacgaggccc tggtcgtcga ctacgagtc ccctgatcc gccgggacct ggacacgggc | 2340 |
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| gaggcgcacg tggccatgct gtccacggtg gtgaaccggc tcggctgcaa gatcgggccg | 2460 |
| gacgccgacc cggacgacgt cctgcgggtg tgcgaggcgc tcgaccgcg gcgcgatccg | 2520 |
| ggcgtctcg tctgatccc gcggatgggc cgggaccgga tccgggagtc cctgccgccg | 2580 |
| atcgtccgcg cgggtgtgaa cgcggggcac cccgtgctct ggctgagcga tccatgcac | 2640 |
| ggcaacaccg tcaaggcctc ggtcggcctg aagacgcgcc acctctccga cgtggtcacc | 2700 |
| gaggcgctgt ggttcgcga catcctcgac cagcagcggc agcacgccgc cgggctgcac | 2760 |
| atcgaggtcg ccgccaccga cgtgaccgag tgcgtcggcg gttcgggtggc cggcgaggag | 2820 |
| gacctgggcg ggcactacac ctcgtgtgc gaccgcggc tcaaccggg tcaggccacc | 2880 |
| gagctgatcg aagcgtgggc caaggacacc gcgacggtcg gcccgggacc gcggcgctcc | 2940 |
| ggcccttcgg cgcgccgga ggtcgccgcc tgacgtcgcc ggtctttgcg ccggccgttt | 3000 |
| ccgaactgcg ggaaaattga cagaaggaga cctgccggag caaattcggc caggctagcc | 3060 |
| gcgcgtagt tcgtcgtcca ctacttgct gggtagtgct aactaccgt gccgggaccg | 3120 |
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| gatcgggtgac gcgcgtacct catcctatcc gcaactgaatc ctgtctcagc tgaagcgagt | 3240 |
| gtttccaatg tggggcagct caaacacgct ggaagtgaag ggcaacgacg agagattccc | 3300 |
| cctgcccgat gcagctacgg aggatcggtc tgtgcttggc gagacggttc cggtttcgcg | 3360 |
| gctgctgccc ggtgactccc cgcggtggc gggcgagaac gtcgagcaca tccggctgct | 3420 |
| ggccgcgatg cacgacctc cgccgatcct ggtgcaacgc ggcacgatgc gggtagtcga | 3480 |

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| cgccatgcac | cggctgcggg | ccgccaagct | gcgcgccgac | gagaccgtgc | gggtgacgtt | 3540 |
| cttcgacggg | gacgacgccg | cggcgttcct | gctctcggtc | gacgccaaca | tcaaacacgg | 3600 |
| gctgccgttg | tcccgcgccg | accgggaggg | cgccgccacc | cgcatcctgc | ggttgtatcc | 3660 |
| gcagtggtcg | gaccgcgccg | tcgccgcggc | ggccgggctg | tcaccgacca | cggcgagcgg | 3720 |
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| ccagccctcc | gtgccgcctg | tcgactggcc | ggcggtacgg | ggcaacctga | tccgggaccc | 4080 |
| cgcggtgaag | tacgccgagc | tgggcccggc | cttcgtccgc | tgggcccagc | ggcacgtggt | 4140 |
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| ccttcgatcc | gctgccctca | tttttcgggt | agcacatttt | tgcgggcggt | caatggagag | 4440 |
| gagaattccc | ggtgaacatt | ctgaggcgcc | cgcggaacgc | gcattctcgg | ggtgtcgcgg | 4500 |
| ccgtcgcgcg | ggcgatcgcc | ctgggtggcg | cgctgacaaa | cgggtgtggc | gctgccccgc | 4560 |
| aggcgccgac | cttcgacctc | gacaacggga | acgccctgac | cgacgtcatc | taccggcccc | 4620 |
| tcaacaccga | gccgcgggtc | gagtacagcg | gccggcccgg | gtcctggggc | gcggaccgcg | 4680 |
| ccatgctcat | cgaactgccg | tggttcgacg | ccctggcgcc | gtaccacccc | accgcggctg | 4740 |
| gcattctctc | caccatcgcc | cgccgtcccc | ccgaggagca | cacgacgcgc | aacaagaaca | 4800 |
| tcgcccgtcat | ctactcggcc | tacacctcgc | tcagcaagct | ctacccccag | cacgaggcga | 4860 |
| cctggcagcg | gatgatggcc | accgcggggc | tggacccggc | cgtcaccgcg | gaggaccgga | 4920 |
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<210> 65
<211> 532
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 65

Val Asp Pro Val Pro Val Leu Val Val Gly Ala Gly Pro Val Gly Met
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Val Thr Ala Leu Ala Leu Ala Arg His Gly Val Ala Cys Val Leu Val
20 25 30

Asp Gln Gly Phe Glu Thr Ser Val His Pro Lys Leu Asp Tyr Val Asn
35 40 45

Ala Arg Ser Met Glu Phe Leu Arg Gln Phe Gly Leu Ala Asp Asp Val
50 55 60

Arg Ala Ala Gly Val Ala Pro Glu His Arg Ala Asp Val Ile Trp Ser
65 70 75 80

Thr Gly Leu Ala Gly Glu Pro Ile Thr Arg Trp Gly Leu Pro Ser Val
85 90 95

Thr Gln Glu Trp Arg Arg Ile Ala Glu His Asn Asp Gly Thr Gln Pro
100 105 110

Ala Glu Pro Gly Gln Arg Ile Ser Gln Ile Asp Leu Glu Pro Val Leu
 115 120 125
 Arg Ala Arg Cys Arg Arg Glu Pro Leu Val Asp Leu Arg Leu Gly Val
 130 135 140
 Arg Phe Asp Ser Leu Thr Gln Asp Asp Ala Gly Val Thr Ser Val Leu
 145 150 155 160
 Ala Asp Asp Thr Gly Gly Glu Val Arg Val Arg Ser Glu Tyr Val Val
 165 170 175
 Gly Cys Asp Gly Ala Ser Ser Gln Val Arg Arg Ala Val Gly Ile Gly
 180 185 190
 Glu Glu Gly Phe Asp Val Pro Gly Leu Pro Gly Ala Phe Met Val His
 195 200 205
 Phe Thr Ser Arg Asp Leu Asp Ser Leu His Arg His Gly Arg Phe Trp
 210 215 220
 His Tyr Phe Ala Phe Arg Tyr Val Ile Ile Ala Gln Asp Glu Val Asp
 225 230 235 240
 Thr Trp Thr Ala His Val Asn Gly Val Asp Pro Asn Glu Phe Asp Glu
 245 250 255
 Pro Pro Ala Asp Pro Glu Ala Phe Leu Leu Asp Thr Ile Arg Thr Glu
 260 265 270
 Leu Arg Ile Asp Lys Val Leu Leu Thr Ser Arg Trp Arg Pro Gly Phe
 275 280 285
 Met Leu Ala Asp Arg Tyr Arg Ala Gly Arg Val Leu Leu Ala Gly Asp
 290 295 300
 Ser Ala His Arg Met Phe Pro Thr Gly Ala Tyr Gly Met Asn Thr Gly
 305 310 315 320
 Ile Gly Asp Ala Val Asp Val Ala Trp Lys Leu Ala Ala Val Val Arg
 325 330 335
 Gly Phe Gly Gly Pro Gly Leu Leu Asp Ser Tyr Asp Ala Glu Arg Arg
 340 345 350
 Pro Val Gly Arg Arg Asn Met Arg Thr Ser His Arg His Leu Gly Val
 355 360 365
 His Leu Arg Ala Gly Glu Leu Leu Arg Gly Gly Ala Pro Leu Pro Ser
 370 375 380
 Val Ala Ala Phe Leu Asp Ala Glu Arg Gly Glu Asn Glu Tyr Arg Gly
 385 390 395 400
 Ile Glu Leu Gly Tyr Arg Tyr Ser Gly Ser Pro Val Leu Trp Pro Glu
 405 410 415

Gly Pro Gly Glu Pro Ser Asp Asp Pro Arg Ala Tyr Ala Pro Thr Thr
 420 425 430
 Trp Pro Gly Ala Arg Pro Pro Ser Leu Leu Leu Ser Asp Gly Gln Gln
 435 440 445
 Ile Phe Asp Arg Phe Asp Pro Ala Ser Phe Thr Leu Val Asp Phe Thr
 450 455 460
 Gly Asp Gly Ala Ala Gly Pro Leu Leu Ala Ala Ala Ala Ala Arg Gly
 465 470 475 480
 Leu Pro Val Thr His Thr Val Val Thr Asp Pro Arg Ala Arg Glu Leu
 485 490 495
 Trp Glu Arg Asp Leu Val Leu Leu Arg Pro Asp His His Val Ala Trp
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 Arg Gly Gly Gly
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<210> 66
 <211> 1599
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 66
 gtggatccgg taccggttct ggtcgtgggc gcgggcccgg tcggcatggt caccgcgctg 60
 gcgctcgccc gtcacggcgt cgctgcgctc ctgcgcgacc agggcttcga gacgtcggtc 120
 catccaagc tggactacgt caacgcccgc agcatggagt tcctccgcca gtteggcctc 180
 gccgacgacg tccgtgccgc cggcgtcgcg cccgagcacc gggccgacgt catctggctg 240
 accggcctgg ccggtgagcc gatcaccagg tgggggctgc cctcggtgac gcaggagtgg 300
 cgccgcacgc ccgagcaca cgacggcacc cagccggccg agcccgcca gcggatctcc 360
 cagatcgacc tggaaccggt cctgcggggc cgctgccggc gggagcccct tgtcgacctg 420
 cgctcggcg tacggttcga ctgcgtgacc caggacgacg cgggggtcac cagcgtcctc 480
 gccgacgaca ccggcgggca ggtccgggtg cggtcggagt acgtggtcgg gtgcgacggc 540
 gcgtcgagcc aggtccgccc ggccgtgggc atcggtgagg aggggttcga cgtgcccggc 600
 ctgccgggcg cttcatggt gcacttcacc agccgggacc tggacagcct gcaccggcac 660
 ggccggttct ggcaactatt cgcgttcgga tacgtgatca tcgcccagga cgaggtcgac 720
 acctggaccg cgcacgtcaa cggcgtcgac ccgaacgagt tcgacgagcc gccggccgac 780
 ccggaggcgt tcctgctcga cagatccgc accgagctgc ggatcgacaa ggtgctgctc 840

acctcgcgct ggcgtcccgg cttcatgctc gccgacaggt accgcgccgg ccgggtgctg 900
 ctgcgccggtg actcggccca ccggatgttc cccaccggcg cgtacggcat gaacaccggc 960
 atcggcgacg ccgtcgacgt ggcttgaag ctggccgctg tcgtccgggg cttcggcggc 1020
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 acctcgcacc ggcacctggg cgtgcacctg cgggcgggcg agctcctgcg cggcggcgcc 1140
 ccgctgccgt ccgtcgcggc cttcctcgac gccgagcggg gcgagaacga gtaccggggg 1200
 atcgagctcg gctaccgcta ctccggctcg ccggtgctct ggccggaggg cccgggggag 1260
 ccctcggacg acccgcgggc gtacgccccg acgacctggc ccggcgcccc tccgcccgagc 1320
 ctctgctga gcgacgggca gcagatcttc gaccggttcg acccggcctc gttcaccctc 1380
 gtggacttca ccggtgacgg cgccgccggt ccgctgctgg cggcggcggc cgcgcggggg 1440
 ctcccgtca cccacaccgt ggtgaccgac cccggggctc gtgagctgtg ggaacgcgac 1500
 ctgctctgc tgcggccgga ccaccacgtc gcctggcggg gaaacaccgt gccgccggac 1560
 cccgacgccg tgggtccagc cgtgcggggg gccggatag 1599

<210> 67
 <211> 423
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 67

Met Gln Gln Ser Gly Ser Thr Ala Glu Arg Ser Pro Leu Gly Pro Trp
 1 5 10 15

Glu Gly Met Pro Ala Val Gln Gln Pro Asp Trp Gln Asp His Pro Ala
 20 25 30

Tyr Ala Glu Thr Cys Gln Ala Leu Ala Ser Ala Pro Pro Leu Val Pro
 35 40 45

Pro Gly Glu Val Arg Gly Phe Arg Gln Leu Leu Ser Glu Leu Ala Ser
 50 55 60

Thr Asp Gly Leu Leu Leu Gln Leu Gly Asp Cys Ala Glu Ser Leu Tyr
 65 70 75 80

Glu Cys Thr Pro Arg His Thr Ser Asp Lys Ile Glu Val Ile Asp Arg
 85 90 95

Leu Gly Asp Arg Leu Ser Glu Leu Thr Gly Arg Asn Val Leu Arg Val
 100 105 110

Gly Arg Met Ala Gly Gln Phe Ala Lys Pro Arg Ser Gln Ala Thr Glu

| 115 | 120 | 125 |
|--|-----|-----|
| Trp His Asp Ala Leu Ser Ile Pro Ser Phe Arg Gly His Met Ile Asn 130 135 140 | | |
| Ser Glu Leu Ala Ala Pro Gly Thr Arg Lys Ala Asp Pro Arg Arg Met 145 150 155 160 | | |
| Trp Trp Ala Tyr Glu Ala Ser Asp Arg Val Gln Arg Val Leu Arg Ala 165 170 175 | | |
| His Arg Glu Gly Asn Arg Arg Ala Ala Arg Thr Glu Gly Pro Trp Ser 180 185 190 | | |
| Ser His Glu Ala Leu Val Val Asp Tyr Glu Ser Arg Leu Ile Arg Arg 195 200 205 | | |
| Asp Pro Asp Thr Gly Glu His Tyr Leu Ala Ser Thr His Leu Pro Trp 210 215 220 | | |
| Val Gly Glu Arg Thr Arg Arg Ser Ala Glu Ala His Val Ala Met Leu 225 230 235 240 | | |
| Ser Thr Val Val Asn Pro Val Gly Cys Lys Ile Gly Pro Asp Ala Asp 245 250 255 | | |
| Pro Asp Asp Val Leu Arg Val Cys Glu Ala Leu Asp Pro Arg Arg Asp 260 265 270 | | |
| Pro Gly Arg Leu Val Leu Ile Pro Arg Met Gly Arg Asp Arg Ile Arg 275 280 285 | | |
| Glu Ser Leu Pro Pro Ile Val Arg Ala Val Val Asn Ala Gly His Pro 290 295 300 | | |
| Val Leu Trp Leu Ser Asp Pro Met His Gly Asn Thr Val Lys Ala Ser 305 310 315 320 | | |
| Val Gly Leu Lys Thr Arg His Leu Ser Asp Val Val Thr Glu Ala Leu 325 330 335 | | |
| Trp Phe Arg Asp Ile Leu Asp Gln Gln Arg Gln His Ala Ala Gly Leu 340 345 350 | | |
| His Ile Glu Val Ala Ala Thr Asp Val Thr Glu Cys Val Gly Gly Ser 355 360 365 | | |
| Val Ala Gly Glu Glu Asp Leu Ala Arg His Tyr Thr Ser Leu Cys Asp 370 375 380 | | |
| Pro Arg Leu Asn Pro Gly Gln Ala Thr Glu Leu Ile Glu Ala Trp Ala 385 390 395 400 | | |
| Lys Asp Thr Ala Thr Val Gly Pro Gly Pro Arg Arg Ser Gly Pro Ser 405 410 415 | | |
| Ala Arg Pro Glu Val Ala Ala | | |

420

<210> 68
 <211> 1272
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 68
 atgcagcaat ccggttcaac ggcggaacgc agcccactcg ggcctgaggga gggcatgccg 60
 gcggtccagc aaccggactg gcaggaccac ccggcgtagc cggagacctg tcaggcggtg 120
 gcgtcggccc cgccgctggt cccacccggg gaggtacggg ggttcgggca gctgttgctg 180
 gagctggcgt cgaccgacgg gtcctctgctg cagttgggcg actgcgccga gagcctctac 240
 gagtgcaccc cccggcacac ctccgacaag atcgaggtca tcgaccggct gggggaccgg 300
 ctccgagcgc tcaccgggcg caacgtgctg cgggtgggccc ggatggccgg gcagttcgcc 360
 aagccccggt cgcaggcgac ggagtggcac gacgcgctga gcatcccctc cttccgcggc 420
 cacatgatca attccgagct ggccgcgccc ggtacgcgca aggccgaccc tcgccgcatg 480
 tggtagggcgt acgaggcgag cgaccgggtg cagcgggtcc tgcgcgccca ccgggagggc 540
 aaccggcggtg ccgcgcggac cgagggggccg tggtagagcc acgaggccct ggtcgtcgac 600
 tacgagtcct gcctgatccg ccgggacccg gacacgggcg agcactacct ggcgtcgacc 660
 cacctgccgt gggtaggggga gcggaccgcg cggtagcccg aggcgcacgt ggccatgctg 720
 tccacggtgg tgaaccgggt cggctgcaag atcggggccg acgccgaccc ggacgacgtc 780
 ctgcgggtgt gcgaggcgct cgaccgcgcg cgcgatcccg gccgtctcgt cctgatcccg 840
 cggatgggccc gggaccggat ccgggagtcg ctgcgcgcca tcgtccgcgc ggtggtgaac 900
 gcggggcacc ccgtgctctg gctgagcgat cccatgcacg gcaacaccgt caaggcctcg 960
 gtcggcctga agacgcgcca cctctccgac gtgggtcaccg aggcgctgtg gttccgcgac 1020
 atcctcgacc agcagcggca gcacgccgccc gggctgcaca tcgaggtcgc cgccaccgac 1080
 gtgaccgagt gcgtcggcgg ttcggtggcc ggcgaggagg acctggcgcg gcactacacc 1140
 tcgctgtgcg acccgcggtc caaccgggtc caggccaccg agctgatcga agcgtgggccc 1200
 aaggacaccg cgacgggtcgg cccgggaccg cggcgctccg gcccttcggc gcggccggag 1260
 gtcgccgcct ga 1272

<210> 69
 <211> 340
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 69

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Gly | Ser | Ser | Asn | Thr | Leu | Glu | Val | Lys | Gly | Asn | Asp | Glu | Arg | 1 | 5 | 10 | 15 |
| Phe | Pro | Leu | Pro | Asp | Ala | Ala | Thr | Glu | Asp | Arg | Ser | Val | Leu | Gly | Glu | 20 | 25 | 30 | |
| Thr | Val | Pro | Val | Ser | Ala | Leu | Leu | Pro | Gly | Asp | Ser | Pro | Arg | Leu | Ala | 35 | 40 | 45 | |
| Gly | Glu | Asn | Val | Glu | His | Ile | Arg | Leu | Leu | Ala | Ala | Met | His | Asp | Leu | 50 | 55 | 60 | |
| Pro | Pro | Ile | Leu | Val | Gln | Arg | Gly | Thr | Met | Arg | Val | Ile | Asp | Gly | Met | 65 | 70 | 75 | 80 |
| His | Arg | Leu | Arg | Ala | Ala | Lys | Leu | Arg | Gly | Asp | Glu | Thr | Val | Arg | Val | 85 | 90 | 95 | |
| Thr | Phe | Phe | Asp | Gly | Asp | Asp | Ala | Ala | Ala | Phe | Leu | Leu | Ser | Val | Asp | 100 | 105 | 110 | |
| Ala | Asn | Ile | Lys | His | Gly | Leu | Pro | Leu | Ser | Arg | Ala | Asp | Arg | Glu | Ala | 115 | 120 | 125 | |
| Ala | Ala | Thr | Arg | Ile | Leu | Arg | Leu | Tyr | Pro | Gln | Trp | Ser | Asp | Arg | Ala | 130 | 135 | 140 | |
| Val | Ala | Ala | Ala | Ala | Gly | Leu | Ser | Pro | Thr | Thr | Ala | Ser | Gly | Ile | Arg | 145 | 150 | 155 | 160 |
| Arg | Arg | Leu | Leu | Gln | Pro | Ala | Ala | Arg | Glu | Gly | Ser | Arg | Val | Gly | Arg | 165 | 170 | 175 | |
| Asp | Gly | Arg | Val | Arg | Pro | Leu | Asp | Gly | Ser | Ala | Gly | Arg | Arg | Arg | Ala | 180 | 185 | 190 | |
| Ser | Ala | Val | Ile | Ala | Leu | Arg | Pro | Asp | Ala | Pro | Leu | Arg | Ala | Ile | Ala | 195 | 200 | 205 | |
| Gln | Glu | Ala | Gly | Val | Ser | Val | Gly | Thr | Ala | Arg | Asp | Val | Arg | Ala | Arg | 210 | 215 | 220 | |
| Leu | Gln | Ala | Gly | Arg | Asp | Pro | Val | Leu | Thr | Ser | Gln | Arg | Pro | Ala | Ala | 225 | 230 | 235 | 240 |
| Glu | Pro | Glu | Pro | Ala | Ala | Asp | Asp | Gly | Pro | Glu | Ala | Arg | Arg | Arg | Arg | 245 | 250 | 255 | |
| Leu | Gly | Gln | Pro | Ser | Val | Pro | Pro | Val | Asp | Trp | Pro | Ala | Val | Arg | Gly | 260 | 265 | 270 | |
| Asn | Leu | Ile | Arg | Asp | Pro | Ala | Val | Lys | Tyr | Ala | Glu | Leu | Gly | Arg | Ala | 275 | 280 | 285 | |

Phe Val Arg Trp Ala Asp Gly His Val Val Asp Pro Ala Ala Trp Arg
 290 295 300

Glu Phe Val Asp Ala Val Pro Pro Tyr Trp Arg Lys Ser Val Ala Glu
 305 310 315 320

Leu Ala Arg Ser Cys Ala Ser Ala Trp Leu Ala Phe Ala Gln Glu Leu
 325 330 335

Glu Asp Arg Ala
 340

<210> 70
 <211> 1023
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 70
 atgtggggca gctcaaacac gctggaagtg aagggcaacg acgagagatt ccccttgccc 60
 gatgcagcta cggaggatcg gtctgtgctt ggcgagacgg ttccggtttc cgcgctgctg 120
 cccggtgact ccccgcggtt ggcgggagag aacgtcgagc acatccggct gctggccgcg 180
 atgcacgacc tcccgcgat cctggtgcaa cgcggcacga tgcgggtgat cgacggcatg 240
 caccggctgc gggccgcaa gctgcgcggc gacgagaccg tgcgggtgac gttcttcgac 300
 ggggacgacg ccgcggtgtt cctgctctcg gtcgagcca acatcaaaca cgggctgccg 360
 ttgtcccgcg ccgaccggga ggcgcgcgc acccgcatcc tgcggttgta tccgcagtgg 420
 tcggaccgcg ccgtcgccgc ggcggccggg ctgtcaccga ccacggcgag cggcatccgg 480
 cgccgcctgc tgcaaccggc ggcgcgggag ggcagccggg tgggacggga cgggcgggtg 540
 cgcccgtgg acggctcggc gggccgacgg cgggccagcg cggtcacgc gctccggccg 600
 gacgcgcccc tgcgtgccat cgcgcaggag gccggggtgt cggtgggcac ggcgcgggac 660
 gtgcgcgccc ggttgccaggc gggccgggac cccgtcctga cctgcagcg accggcggcc 720
 gagcccgagc cggccgcca cgacgggccc gaggcgcgca gacgccggtt cggccagccc 780
 tccgtgccgc ctgtcgactg gccggcggtg cggggcaacc tgatccggga ccccgcggtg 840
 aagtacgccc agctgggccc ggccttcgtc cgctgggccc acgggcacgt ggtggatccg 900
 gggcctggc gcgagttcgt cgacgccgtg ccgccgtact ggcgcaaata ggtggccgag 960
 ctggcccgtt cgtgcgccag cgcctggctg gcgttcgccc aggaactgga ggaccgggcg 1020
 tga 1023

<210> 71
 <211> 493

<212> PRT

<213> Micromonospora sp. strain 046-ECO11

<400> 71

Val Asn Ile Leu Arg Arg Pro Arg Lys Arg His Leu Gly Gly Val Ala
1 5 10 15
Ala Val Ala Ala Ala Ile Ala Leu Val Ala Ser Leu Thr Asn Gly Val
20 25 30
Ala Ala Ala Pro Gln Ala Pro Thr Phe Asp Leu Asp Asn Gly Asn Ala
35 40 45
Leu Thr Asp Val Ile Tyr Pro Ala Leu Asn Thr Glu Pro Arg Val Glu
50 55 60
Tyr Ser Gly Arg Pro Gly Ser Trp Ala Ala Asp Arg Ala Met Leu Ile
65 70 75 80
Glu Leu Pro Trp Phe Asp Ala Leu Ala Ala Tyr His Pro Thr Ala Val
85 90 95
Gly Ile Phe Ser Thr Ile Gly Arg Arg Pro Ala Glu Glu His Thr Thr
100 105 110
Arg Asn Lys Asn Ile Ala Val Ile Tyr Ser Ala Tyr Thr Ser Leu Ser
115 120 125
Lys Leu Tyr Pro Gln His Glu Ala Thr Trp Gln Arg Met Met Ala Thr
130 135 140
Ala Gly Leu Asp Pro Ala Val Thr Ala Glu Asp Arg Thr Thr Ala Ser
145 150 155 160
Gly Ile Gly Ile Leu Ala Ser Lys Asn Ala Met Ala Ala Arg Arg Asn
165 170 175
Asp Gly Thr Asn Arg Asp Gly Asp Ala Gly Gly Arg Arg Tyr Asn Arg
180 185 190
Glu Pro Tyr Ala Asp His Thr Gly Tyr Arg Pro Val Asn Ser Pro Tyr
195 200 205
Glu Leu Arg Phe Pro Ser Arg Trp Gln Pro Asn Thr Ile Ser Lys Arg
210 215 220
Glu Val Val Leu Thr Gln Glu Phe Ala Thr Pro Gln Phe Gly Arg Val
225 230 235 240
Lys Pro Ile Thr Phe Glu Arg Pro Glu Gln Phe Arg Leu Thr Pro Pro
245 250 255
Pro Asn His His Leu Leu Asn Pro Lys Gly Tyr Arg Lys Gln Ala Asp
260 265 270
Glu Val Leu Arg Ala Ser Ala Gly Leu Asp Asp Arg Lys Lys Met Ser

| 275 | | | | | | | | | | 280 | | | | | | | | | | 285 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| Ala | Glu | Ile | Phe | Ser | Asp | Asn | Ile | Thr | Pro | Tyr | Gly | Ala | Ile | Ala | His | | | | | | | | | | | | | | | |
| 290 | | | | | | 295 | | | | | 300 | | | | | | | | | | | | | | | | | | | |
| Thr | Leu | Leu | Arg | Gly | Arg | Tyr | Asn | Thr | Glu | Asp | Ser | Val | Arg | Phe | Ile | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | | | | | | | | | | | |
| Val | Met | Thr | Asp | Val | Ala | Gly | Phe | Asp | Val | Ala | Ile | Ala | Ser | Trp | Tyr | | | | | | | | | | | | | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | | | | | | | | | | | | | |
| Tyr | Met | Arg | Lys | Tyr | Asp | Ser | Val | Gln | Pro | Phe | Ser | Ala | Ile | Arg | His | | | | | | | | | | | | | | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | | | | | | | | | | | | | | |
| Leu | Tyr | Pro | Asn | Lys | Lys | Leu | Thr | Ala | Trp | Gly | Gly | Pro | Gly | Arg | Gly | | | | | | | | | | | | | | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | | | | | | | | | | | | | | |
| Thr | Val | Asn | Asp | Ile | Thr | Gly | Thr | Gln | Trp | Arg | Ser | Tyr | Leu | Ser | Ser | | | | | | | | | | | | | | | |
| | | 370 | | | | 375 | | | | | 380 | | | | | | | | | | | | | | | | | | | |
| Val | Ala | Ile | Ala | Ala | Pro | Asp | Tyr | Pro | Ser | Val | Asn | Ala | Ala | Val | Cys | | | | | | | | | | | | | | | |
| 385 | | | | | 390 | | | | | 395 | | | | 400 | | | | | | | | | | | | | | | | |
| Val | Ala | Tyr | Ala | Gln | Val | Ala | Arg | Arg | Phe | Thr | Gly | Thr | Asp | Lys | Leu | | | | | | | | | | | | | | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | | | | | | | | | | | | | | |
| Thr | Val | Val | Ile | Pro | Val | Arg | Lys | Gly | Ser | Ser | Ile | Val | Glu | Pro | Gly | | | | | | | | | | | | | | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | | | | | | | | | | | | | | |
| Val | Thr | Pro | Ala | Ala | Asp | Met | Met | Leu | Thr | Trp | Asn | Ser | Tyr | Ser | Glu | | | | | | | | | | | | | | | |
| | | 435 | | | | 440 | | | | | | 445 | | | | | | | | | | | | | | | | | | |
| Trp | Ala | Ala | Glu | Cys | Gly | Gln | Ser | Arg | Val | Trp | Ala | Gly | Glu | Asn | Phe | | | | | | | | | | | | | | | |
| | | 450 | | | | 455 | | | | | 460 | | | | | | | | | | | | | | | | | | | |
| Pro | Ala | Ser | Val | Ala | Ala | Ala | Asp | Gln | Tyr | Ala | Pro | Gln | Ile | Gly | Asp | | | | | | | | | | | | | | | |
| 465 | | | | | 470 | | | | | 475 | | | | 480 | | | | | | | | | | | | | | | | |
| Arg | Ala | Phe | Asp | Phe | Val | Gln | Ser | Lys | Leu | Asn | Gly | Arg | | | | | | | | | | | | | | | | | | |
| | | | | 485 | | | | | 490 | | | | | | | | | | | | | | | | | | | | | |

<210> 72

<211> 1482

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 72

| | |
|--|-----|
| gtgaacattc tgaggcggcc gcggaaacgg catctcgggg gtgtcgcggc cgtcgccgcg | 60 |
| gcgatcgccc tgggtggcgtc gctgacaaac ggtgtggcgg ctgccccgca ggcgccgacc | 120 |
| ttcgacctcg acaacgggaa cgccctgacc gacgtcatct acccggccct caacaccgag | 180 |
| ccgcgggtcg agtacagcgg ccggccccgg tcttggggccg cggaccgcgc catgctcatc | 240 |
| gaactgccgt ggttcgacgc cctggcgggc taccacccca ccgcggtcgg catcttctcc | 300 |

| | |
|---|------|
| accatcggcc gccgtcccgc cgaggagcac acgacgcgca acaagaacat cgccgtcatc | 360 |
| tactcggcct acacctcgct cagcaagctc tccccccagc acgaggcgac ctggcagcgg | 420 |
| atgatggcca ccgcgggcct ggacccggcc gtcaccgcgg aggaccggac caccgccagc | 480 |
| ggcatcggca tcctcgctc gaagaacgcg atggcggcgc gccggaacga cggcacgaac | 540 |
| cgcgacggcg acgcgggcgg ccgtcgctac aaccgtgagc cgtacgccga ccacaccggc | 600 |
| taccggccgg tcaacagccc gtacgagctg cgcttcccgt cgcgctggca gccgaacacc | 660 |
| atctccaagc gcgaggtcgt cctgacgcag gagttcgcga cgccccagtt cggccgggtc | 720 |
| aagccgatca ccttcgagcg gcccgagcag ttccgggtca ccccgccgcc gaaccaccac | 780 |
| ctgttgaacc cgaagggcta ccggaagcag gccgacgagg tgctgcgcgc ctcggcgggc | 840 |
| ctggacgacc gcaagaagat gagcgcggag atcttcagcg acaacatcac gccgtacggc | 900 |
| gccatcgcgc acacgtcct gcggggccgg tacaacaccg aggactccgt ccggttcac | 960 |
| gtgatgactg acgtcgccgg gttcgacgtg gcgatcgct cctggtacta catgcgcaag | 1020 |
| tacgactcgg tgcagccgtt cagcgcgac cgccacctgt acccgaacaa gaagctgacc | 1080 |
| gcgtggggcg gcccgggcgg gggcaccgtc aacgacatca ccggcaccca gtggcgcagc | 1140 |
| tacctcagct cggtcgccat cgcggtccg gattaccggt cggtaaacgc ggcggtctgc | 1200 |
| gtcgcctacg ccaggtcgc gcgccggttc accggcacgg acaagctgac cgtcgtgatc | 1260 |
| ccggtccgca agggctcctc gatcgtggaa ccgggcgtga ccccgccgc cgacatgatg | 1320 |
| ctcacctgga acagctactc ggagtgggcc gccgagtgcg ggcagagccg ggtctgggcc | 1380 |
| ggcgagaact tccccgcctc ggtcgcggcc gccgaccagt acgcgccgca gatcggcgac | 1440 |
| cgtgccttcg acttcgtcca gagcaagctg aacgggcgct ga | 1482 |

<210> 73

<211> 9762

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 73

| | |
|---|-----|
| cagccacggc gttccgaccc cccgcaagat ggcttgata gcaaggatc ttgcgatgca | 60 |
| tggacggggc acgtgagcgg atcactacga acatccgcaa gggcgtgctg gagtactgcg | 120 |
| tgctcgccct gctctcgcg cgcgacatgt acggcctgga actggccgac tggtcgcgg | 180 |
| tccgcggtct gaccgcgagc gagggcagcc tgtatccgct gctcgccgc atgcggcagg | 240 |
| ccggctccgt gcagaccgg tgggtggccc ccgagcaggg gcacgcccgg cgggtactacg | 300 |

| | |
|--|------|
| cgatcaccga ccagggggcgg gcgcacctgc ggggtgttcgc ggcgggtgtgg caggagatcc | 360 |
| agccgcacgt ggacgacctg atgggggagg aagcatgagc gacgacggcc tcccggaggc | 420 |
| ggcgtggacc tatctgcgcg cgctcgacgc ggagttgtcc gacgtcccgt ccggcacggc | 480 |
| ggaggagatc gtcgcggatg tccgcgcgca catcgccgac gccctcgaca gcggacggag | 540 |
| cgcccacgag atcctcgccg gcctcggcgc cgcgcgggac gtggcccggc aggcgcgcga | 600 |
| ggagctgggg ctgccggccc aggaccgcc ggcccgggccc ggccggaccc tgtccctggc | 660 |
| cgcggtggcg gtcggcgtgc tgategccgt gtgcgtgagc ttcttctgtc cgtccgcagt | 720 |
| gccggtggag ccgatccagg ccggccccgg cgagcagggc gtctctccgc ggctcggccc | 780 |
| cggaatcgcg ctgctcacgc tgctgcgggc gctcgtcgcg gccgcgcgc tcgtggcgcc | 840 |
| cgcccgggca cgtgccgggg tacggttcgc cggcgcggcg gtcttgacga tgttcgcctg | 900 |
| cgcgccgggc gagacgggccc tgtactactt cccgctcgcg ctgatggcct gggcggcggc | 960 |
| gatcgtgccg tgggccctgc ggcgcggagc cgggtggacgg tggtagcgct atctgaccgg | 1020 |
| tggattcgtg gcgatgcccg gcgtgctggt ggcggtcgcg tcggccgggtg gctcggtcgg | 1080 |
| cgtcggctgg gtcggcgcg cgctgtggat cgccggggcg ctgcggggcg gcgcgctgtg | 1140 |
| cgcttacggg atccggggcg gctacgccgt gaccgcgctg gccggcgcg tcggccatagc | 1200 |
| gctctcgatg gccgagcgcg gcttctctgt cgcgccttc tggctgttcg gcgggctgta | 1260 |
| cctggcgctc ggcgcgcgtg cgtacaccgc ctgcggggcc gtcgacggcg acgccgccgc | 1320 |
| gacgcccggc ccgccggccc ggccggaacc cgcgcgggccc cccggaggct gacccggggg | 1380 |
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<211> 112
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 74

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| Met | Asp | Gly | Ala | Arg | Glu | Arg | Ile | Thr | Thr | Asn | Ile | Arg | Lys | Gly | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Leu | Glu | Tyr | Cys | Val | Leu | Ala | Leu | Leu | Ser | Arg | Arg | Asp | Met | Tyr | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| | | | | | | | | | | | | | | | |
| Leu | Glu | Leu | Ala | Asp | Trp | Leu | Ala | Val | Arg | Gly | Leu | Thr | Ala | Ser | Glu |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| | | | | | | | | | | | | | | | |
| Gly | Ser | Leu | Tyr | Pro | Leu | Leu | Ala | Arg | Met | Arg | Gln | Ala | Gly | Ser | Val |
| | | | 50 | | | | 55 | | | | 60 | | | | |
| | | | | | | | | | | | | | | | |
| Gln | Thr | Arg | Trp | Val | Ala | Pro | Glu | Gln | Gly | His | Ala | Arg | Arg | Tyr | Tyr |
| | | | 65 | | | 70 | | | | 75 | | | | 80 | |
| | | | | | | | | | | | | | | | |
| Ala | Ile | Thr | Asp | Gln | Gly | Arg | Ala | His | Leu | Arg | Val | Phe | Ala | Ala | Val |
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Trp Gln Glu Ile Gln Pro His Val Asp Asp Leu Met Gly Glu Glu Ala
 100 105 110

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 <213> Micromonospora sp. strain 046-EC011

<400> 75
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 <211> 325
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 76

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Leu Asp Ala Glu Leu Ser Asp Val Pro Ser Gly Thr Ala Glu Glu Ile
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Val Ala Asp Val Arg Ala His Ile Ala Asp Ala Leu Asp Ser Gly Arg
 35 40 45

Ser Ala His Glu Ile Leu Ala Gly Leu Gly Ala Ala Arg Asp Val Ala
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Arg Gln Ala Arg Glu Glu Leu Gly Leu Pro Ala Gln Asp Arg Pro Ala
 65 70 75 80

Arg Ala Gly Arg Thr Leu Ser Leu Ala Ala Val Ala Val Gly Val Leu
 85 90 95

Ile Ala Val Cys Val Ser Phe Leu Leu Pro Ser Ala Val Pro Val Glu
 100 105 110

Pro Ile Gln Ala Gly Pro Gly Glu Gln Gly Val Leu Arg Arg Leu Gly
 115 120 125

Pro Gly Ile Ala Leu Leu Thr Leu Leu Pro Ala Leu Val Ala Ala Ala
 130 135 140

Pro Leu Val Ala Pro Ala Arg Ala Arg Ala Gly Val Arg Phe Ala Gly

| | | | |
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| 145 | 150 | 155 | 160 |
| Ala Ala Val Leu Thr Met Phe Ala Cys Ala Ala Gly Glu Thr Gly Leu | 165 | 170 | 175 |
| Tyr Tyr Phe Pro Leu Ala Leu Met Ala Trp Ala Ala Ala Ile Val Pro | 180 | 185 | 190 |
| Trp Ala Leu Arg Arg Gly Ala Gly Gly Arg Trp Trp Arg Tyr Leu Thr | 195 | 200 | 205 |
| Gly Gly Phe Val Ala Met Pro Gly Val Leu Val Ala Val Ala Ser Ala | 210 | 215 | 220 |
| Gly Gly Ser Val Gly Val Gly Trp Val Gly Ala Ala Leu Trp Ile Ala | 225 | 230 | 235 |
| Gly Pro Leu Ala Ala Gly Ala Leu Cys Ala Tyr Gly Ile Arg Ala Gly | 245 | 250 | 255 |
| Tyr Ala Val Thr Ala Leu Ala Gly Ala Leu Ala Ile Ala Leu Ser Met | 260 | 265 | 270 |
| Ala Glu Arg Gly Phe Leu Phe Ala Ala Phe Trp Leu Phe Gly Gly Leu | 275 | 280 | 285 |
| Tyr Leu Ala Leu Gly Ala Ala Ala Tyr Thr Ala Ser Arg Ala Val Asp | 290 | 295 | 300 |
| Gly Asp Ala Ala Ala Thr Pro Gly Pro Pro Ala Arg Pro Glu Pro Ala | 305 | 310 | 315 |
| Pro Ala Pro Gly Gly | 325 | | |

<210> 77

<211> 978

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 77

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<210> 78
<211> 663
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 78

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Leu Asp Glu Arg Phe Leu Pro Val Tyr Gly Glu Thr Gly Asp Gln Ala
35 40 45

Arg Glu Arg Ile Thr Arg Leu Leu Ser Glu Leu Pro Val Glu Leu Gly
50 55 60

Ile Ala Ser Gly Phe Pro Ala Glu Tyr Gly Gly Arg Gly Asp Val Gly
65 70 75 80

Ala Ser Ile Val Ala Thr Glu Met Leu Ala Gln Val Asp Leu Ser Leu
85 90 95

Met Val Lys Ala Gly Val Gln Trp Gly Leu Phe Gly Gly Ala Val Ala
100 105 110

Ala Leu Gly Thr Lys Arg His His Asp Ala Tyr Leu Arg Asp Ile Val
115 120 125

Ala Gly Arg Leu Phe Gly Cys Phe Ala Met Thr Glu Thr Gly His Gly
130 135 140

Ser Asp Val Gln Gln Leu Arg Thr Thr Cys Val Tyr Asp Pro Gln Thr
145 150 155 160

Gln Thr Phe Asp Leu His Thr Pro His Glu Ala Ala Arg Lys Asp Tyr

| 165 | | | | | 170 | | | | | 175 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gly | Asn | Ala | Ala | Arg | Asp | Gly | Arg | Met | Ala | Val | Val | Phe | Ala | Gln |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Val | Thr | Gly | Gly | Arg | Arg | His | Gly | Val | His | Ala | Trp | Leu | Val | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ile | Arg | Asp | Glu | His | Gly | Lys | Pro | Met | Pro | Gly | Val | Thr | Ile | Gly | Asp |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Gly | Pro | Lys | Ala | Gly | Leu | Leu | Gly | Val | Asp | Asn | Gly | Arg | Leu | Ser |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Phe | Asp | His | Val | Arg | Val | Pro | Arg | Glu | Met | Leu | Leu | Asp | Gln | Tyr | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Gln | Val | Ala | Glu | Asp | Gly | Thr | Tyr | Ser | Ser | Pro | Ile | Glu | Asn | Asp | Ser |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Arg | Arg | Phe | Phe | Thr | Met | Leu | Gly | Thr | Leu | Val | Arg | Gly | Arg | Val | Ser |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Val | Gly | Gly | Ala | Ala | Ser | Ala | Ala | Thr | Lys | Ser | Ala | Leu | Ala | Ile | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Val | Arg | Tyr | Gly | Asp | Ile | Arg | Arg | Gln | Phe | Ala | Asp | Ala | Asp | Gly | Asp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Arg | Glu | Val | Leu | Leu | Asn | Asp | Tyr | Leu | Ala | His | Gln | Arg | Lys | Leu | Leu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Pro | Ala | Leu | Ala | Thr | Thr | Tyr | Ala | Leu | Thr | Phe | Ala | Gln | Ala | Glu | Leu |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Val | Ala | Ala | Leu | Asp | Asp | Ile | Gln | Gly | Gly | Asp | Gly | Pro | Val | Asp | Glu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| His | Arg | Gln | Arg | Glu | Leu | Glu | Ser | Arg | Ala | Ala | Gly | Leu | Lys | Ala | Ala |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Gln | Thr | Trp | His | Ala | Thr | Arg | Thr | Ile | Gln | Ile | Cys | Arg | Glu | Ala | Cys |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Gly | Gly | Ala | Gly | Tyr | Leu | Ser | Glu | Asn | Arg | Leu | Pro | Ser | Leu | Lys | Ala |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asp | Thr | Asp | Val | Phe | Thr | Thr | Phe | Glu | Gly | Asp | Asn | Thr | Val | Leu | Leu |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Gln | Leu | Val | Ala | Lys | Gly | Leu | Leu | Thr | Gly | Tyr | Arg | Asp | Glu | Phe | Gly |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ser | Leu | Asp | Gly | Trp | Gly | Arg | Ala | Ser | Phe | Val | Ala | Glu | Gln | Val | Arg |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Glu | Met | Val | Leu | Glu | Arg | Thr | Ala | Ala | Arg | Ala | Leu | Ile | Ala | Arg | Leu |

| | | | |
|-----------------|-------------------------|-----------------|-------------|
| 465 | 470 | 475 | 480 |
| Val Ser Ala Val | Pro Gly Arg Asp Asp | Glu Val Ala Val | Thr Asp Arg |
| | 485 | 490 | 495 |
| Gly Trp Gln Leu | Lys Leu Phe Glu Asp Arg | Glu Glu His Leu | Leu Asp |
| | 500 | 505 | 510 |
| Ser Ala Val Arg | Arg Leu Arg Gly Gly | Ala Ser Thr Lys | Lys Asp Arg |
| | 515 | 520 | 525 |
| Pro Phe Asp Ile | Phe Asn Asp Val Gln Asp | His Val Leu Ala | Val Ala |
| | 530 | 535 | 540 |
| Ala Ala His Ile | Asp Arg Val Thr Leu Glu | Ala Phe Val Ala | Gly Ile |
| | 545 | 550 | 555 |
| Asp Ala Ile Ala | Asp Pro Ala Val Lys Glu | Leu Leu Ser Arg | Val Cys |
| | 565 | 570 | 575 |
| Asp Leu Tyr Ala | Leu Thr Val Ile Glu Ala | Asn Lys Gly Trp | Leu Leu |
| | 580 | 585 | 590 |
| Glu His Gly Arg | Leu Thr Pro Ala Arg | Ser Lys Thr Ile | Thr Ser Val |
| | 595 | 600 | 605 |
| Val Asn Gly Leu | Leu Lys Glu Leu Arg | Pro Asp Met Arg | Thr Leu Val |
| | 610 | 615 | 620 |
| Asp Gly Phe Ala | Ile Pro Asp Ala Trp Leu | His Ala Ala Ile | Leu Arg |
| | 625 | 630 | 635 |
| Glu Glu Pro Val | Arg Gln Glu Thr Met Ala | Ala His Asp Ala | Ala Gly |
| | 645 | 650 | 655 |
| Asp Pro Gln Ala | Val Pro Ala | | |
| | 660 | | |

<210> 79
 <211> 1992
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 79
 atgctcgatc acgcatccgg ccgcatcgac gtcacacgcc tgcgggaagc gctcgacggc 60
 cgggtgggccc aggtccgccg ggcgcaccgc gaacacctcg acgaacgctt cctcccgggtg 120
 tacggcgaga ccggtgacca ggcccgcgag cgcatacccc ggctgctgtc cgaactcccc 180
 gtcgagctgg gcatcgcttc cggtttcccc gccgagtacg gcggccgcgg cgacgtgggc 240
 gcctcgatcg tcgccaccga gatgctggcc caggtggacc tgtcactgat ggtgaaggcc 300
 ggcgtgcagt ggggcctgtt cggcggcgcg gtcgccgccc tcggcacgaa gcggcaccac 360
 gacgcctacc tgcgggacat cgtcgcgggc cggtctttcg gctgcttcgc gatgaccgag 420

| | |
|--|------|
| accggccacg gctcggacgt gcagcaactg cgcaccacct gcgtctacga cccgcagacg | 480 |
| cagaccttcg acctgcacac cccgcacgag gccgcgcgca aggactacat cggcaacgcg | 540 |
| gcccgggacg ggcggtatggc tgtggtgttc gccagctcg tcaccggcgg gcgccgccac | 600 |
| ggggtgcacg cctggctggt gccgatccgc gacgagcacg gcaagccgat gcccggcgtg | 660 |
| accatcggcg acgccggggc caaggccggc ctgctcggcg tggacaacgg gcggctcagc | 720 |
| ttcgaccacg tgcgggtgcc gcgggagatg ctgctggacc agtacgcgca ggtcgccgag | 780 |
| gacggcacgt actccagccc gatcgagaac gactcccggc gcttcttcac catgctgggc | 840 |
| accctggtcc ggggccgggt gagcgtgggc gccgccgcgt cggcggccac caagtcggcg | 900 |
| ctggccatcg cgggtgcgcta cggcgacatc cgccggcagt tcgccgacgc cgacggcgac | 960 |
| cgcgaggtgc tgctcaacga ctacctggcg caccagcgca agctgctgcc cgcgctggcc | 1020 |
| accacgtacg cgctgacctt cgcccaggcg gagctggctg cggcgctcga cgacatccag | 1080 |
| ggcgggcagc ggccggtcga cgagcaccgg cagcgggagc tggagtcccg ggccgccggt | 1140 |
| ctgaaggcgg cgcagacctg gcacgccacc cgcaccatcc agatctgccg ggaggcgtgt | 1200 |
| ggcgggcgccg gctacctgtc cgagaaccgc ctgccagcc tcaaggccga caccgatgtc | 1260 |
| ttcaccacct tcgagggcga caacacggtg ctgctgcaac tggtcgccaa ggggctgctg | 1320 |
| accggctacc gggacgagtt cggctcgctc gacggctggg gacgcgcctc cttcgtggcc | 1380 |
| gagcaggtac gcgagatggt gctggaacgc accgcgcgcg gggcgctgat cgcacgtctg | 1440 |
| gtcagcgccg tgcccgggcg cgacgacgag gtcgccgtca ccgaccgggg ctggcagctc | 1500 |
| aagctcttcg aggaccgca ggagcacctg ctgcacagcg cggtcgcccg cctgcgcggt | 1560 |
| ggcgcgctca ccaagaagga ccgccccttc gacatcttca acgacgtcca ggaccacgtc | 1620 |
| ctcgccgtcg ccgcggcgca catcgaccgg gtgacgctgg aggcgttcgt cgccgggatc | 1680 |
| gacgccatcg ccgaccggc ggtcaaggaa ctgctgtccc gggctctgca cctgtacgcg | 1740 |
| ctcaccgtga tcgaggcgaa caagggtgg ctgctcgagc acggccgggt caccgccgcc | 1800 |
| cgctcgaaga ccataccag cgtggtgaac gggctgctca aggagctgcg cccggacatg | 1860 |
| cgcacgctcg tggacggctt cgccatcccg gacgcgtggc tgcacgggc gatcctgcgc | 1920 |
| gaggagcccg tccggcagga gacgatggcc gcgcacgacg ccgccggcga cccgcaggcc | 1980 |
| gtccccgcct ag | 1992 |

<211> 573
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 80

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Pro | Leu | Pro | Pro | Gly | Ser | Ala | Val | Thr | Ala | Arg | His | Val | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Gln | Ala | Leu | Arg | Arg | Gln | Arg | Arg | Pro | Val | Leu | Ile | Gly | Val | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Leu | Gly | Leu | His | Gln | Val | Thr | Glu | Ala | Leu | Val | Pro | Val | Ala | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Val | Ile | Ile | Asp | Arg | Ala | Val | Val | Thr | Gly | Asp | Pro | Trp | Ala | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Tyr | Ser | Val | Ala | Gly | Leu | Ala | Ala | Leu | Phe | Thr | Val | Leu | Ala | Phe |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Tyr | Arg | Asn | Gly | Ala | Arg | Gln | Ala | Phe | Ala | Ala | Val | Glu | Arg | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | His | Leu | Leu | Arg | Val | Glu | Leu | Ala | Glu | Arg | Ala | Leu | Asp | Pro | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | His | Arg | Ser | Gly | Leu | Arg | Asp | Gly | Glu | Leu | Leu | Ser | Val | Ala | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Asp | Ala | Glu | Leu | Ser | Ala | Tyr | Val | Val | Arg | Val | Ala | Gly | Phe | Gly |
| | 130 | | | | | | 135 | | | | 140 | | | | |
| Val | Ala | Ala | Val | Ser | Ala | Leu | Thr | Val | Ala | Ala | Val | Ala | Leu | Leu | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | Asp | Val | Pro | Leu | Gly | Leu | Gly | Val | Leu | Ile | Gly | Val | Pro | Val | Leu |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Leu | Ala | Leu | Gln | Arg | Met | Ala | Pro | Leu | Leu | Ser | Arg | Arg | Ser | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ser | Gln | Gln | Glu | Ala | Leu | Ala | Glu | Thr | Thr | Ala | Leu | Ala | Val | Asp | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Val | Ser | Gly | Leu | Arg | Val | Leu | Arg | Gly | Ile | Gly | Ala | Gln | His | His | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Gly | Arg | Tyr | Ala | Glu | Ala | Ser | Arg | Arg | Ala | Leu | Ala | Val | Thr | Leu |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Arg | Ala | Ala | Asn | Thr | Lys | Gly | Leu | His | Leu | Gly | Leu | Thr | Thr | Ala | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Asn | Gly | Leu | Phe | Leu | Ala | Ala | Val | Ala | Gly | Val | Ala | Gly | Trp | Leu | Ala |
| | | | 260 | | | | | 265 | | | | | 270 | | |

Leu Arg Gly Arg Leu Thr Ile Gly Glu Leu Val Thr Val Val Gly Leu
 275 280 285
 Ala Gln Phe Val Ala Glu Pro Val Gln Thr Leu Gly Tyr Cys Val Gln
 290 295 300
 Leu Phe Ala Met Ala Arg Ala Ser Ala Ala Arg Val Gly Arg Val Leu
 305 310 315 320
 Gly Ala Glu Pro Leu Thr Arg Pro Gly Ser Ala Pro Arg Pro Asp Arg
 325 330 335
 Thr Asp Gly Pro Arg Leu Val Leu Asp His Val Gly His Ala Ala Leu
 340 345 350
 Asp Gly Val Cys Leu Arg Val Asp Pro Gly Glu Ile Val Gly Val Leu
 355 360 365
 Ala Tyr Asp Pro Ala Asp Ala Asp Ala Leu Val Ala Leu Leu Ser Gly
 370 375 380
 Arg Val Pro Ala Asp Arg Arg Arg Gly Thr Val Arg Val Asp Gly Val
 385 390 395 400
 Pro Ala Asp Asp Leu Asp Val Asp Ala Leu Arg Gly Ala Val Leu Val
 405 410 415
 Glu Pro His Asp Val Thr Leu Phe Glu Gly Thr Val Ala Ala Asn Leu
 420 425 430
 Ala Ala Gly Ser Arg Thr Glu Glu Gly Arg Leu Arg Ala Ala Val Arg
 435 440 445
 Ala Ala Ala Ala Asp Asp Val Val Asp Ala His Pro Gly Gly Leu Gly
 450 455 460
 His Arg Leu Val Glu Arg Gly Ala Asn Leu Ser Gly Gly Gln Arg Gln
 465 470 475 480
 Arg Leu Gly Leu Ala Arg Ala Leu His Ala Asp Pro Pro Val Leu Val
 485 490 495
 Leu His Asp Pro Thr Thr Ala Val Asp Ala Ala Thr Glu Ala Gln Leu
 500 505 510
 Ala Asp Gly Leu Ala Gly Ala Arg Arg Glu Ala Pro Arg Gly Thr Leu
 515 520 525
 Leu Val Thr Ser Ser Pro Ala Leu Leu Arg Ile Thr Asp Arg Val Val
 530 535 540
 Val Ile Ala Asp Gly Arg Val Thr Ala Glu Gly Thr His Glu His Leu
 545 550 555 560
 Leu Ala Thr Asp Ala Arg Tyr Arg Glu Glu Thr Leu Arg
 565 570

<210> 81
 <211> 1722
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 81
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 cgccgccagc gccgcccggg gctgatcggc gtgaccctgc tcgggctgca ccaggtcacc 120
 gagggcgctcg tgccgggtggc gatcggcgctc atcatcgacc gggccgtggt gaccggcgac 180
 ccgtggggcg tcgcgtactc cgtcgccggc ctcgccgccc tgttcaccgt gctggcgctt 240
 gcctaccgca acggcgcccc ccaggcgctt cggcggggtg aacgggaggc gcacctgctg 300
 cgggtcgagc tggccgagcg cgcgctcgac ccgcgcgggc accgctccgg cctgcgcgac 360
 ggcgagctgc tctcggtcgc cgctccgac gccgaactct ccgcgtacgt ggtccgggtg 420
 gccggcttcg gcgtcgccgc ggtgagcgcg ctgaccgtcg cggcggtcgc gctgctggtc 480
 atcgacgtcc cgctcggact cggcggtgctc atcggcgta cgggtgctggt cctggcgctg 540
 caacggatgg cgccgctgct gtccccggcg agcgctccc agcaggaggc cctcgcgagg 600
 accacggcg cgcgctgga cctcgtctcc ggctgcgcg tgctgcgcgg catcggcgcc 660
 cagcaccag cgcggggccg gtacgcccag gccagccgac gcgcctcgc cgtgacgctg 720
 cgcgcccga acaccaagg cctgcacctc gggtcacca ccgcccga cggcctcttc 780
 ctcgccgccc tcgccggggg cgccggctgg ctcgcgctgc gcggccggct caccatcggc 840
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 ggcgccgagc cgctgacccg gccgggcagc gcgccccggc cggaccgcac ggacggggcc 1020
 cggctcgttc tcgaccacgt cggccacgcc gcgctggacg ggggtgtgct gcgcgtcgac 1080
 ccgggagaga tcgtcggcgt cctggcgta caccggccg acgcggacgc gctggtggcg 1140
 ctgctgtccg ggcgggtgcc cgcggaccgg cgccggggca cggtagcgt cgacggggta 1200
 cccgccgacg acctggacgt cgacgcgctg cgcggcgccg tctggtcga gccgcacgac 1260
 gtgacgctgt tcgaggggaa cgtggccgcc aacctcgcc cggggagcag gaccgaggag 1320
 gggcgccctg gcgcccgggt ccgggcggcc gcggcgagc acgtggtgga cgcgcacccc 1380
 ggcggcctcg gccaccggct cgtcgagcgg ggcgccaacc tctccggcg gcagcgccag 1440
 cggctcgggc tggcgcgggc gctgcacgcc gaccgcccg tgctggtgct gcacgacccc 1500
 accaccgccg tggacgcggc caccgaggcc caactcgcc acggactggc cggcgcgcg 1560

cgcggaagcgc cccgggggcac gctgctggtc accagcagcc ccgcccctgct gcggatcacc 1620
gaccgggtgg tggatgatcgc cgacggccgg gtgaccgccc aggggacgca cgagcacctg 1680
ctggccaccg acgcccgccta ccgcgaggag acaactgcggt ga 1722

<210> 82
<211> 596
<212> PRT
<213> Micromonospora sp. strain 046-EC011

<400> 82

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Ala | Asp | Pro | Arg | Thr | Ala | Glu | Pro | Thr | Arg | Val | Leu | Leu | Pro | 1 | 5 | 10 | 15 |
| Thr | Ala | Thr | Ala | Arg | Arg | Thr | Trp | Thr | Thr | Leu | Gly | Ala | Glu | Phe | Arg | 20 | 25 | 30 | |
| Arg | Arg | Pro | Gly | Leu | Ser | Ala | Ala | Ala | Thr | Ala | Val | Leu | Val | Ala | Ala | 35 | 40 | 45 | |
| Ala | Thr | Gly | Gly | Leu | Val | Ala | Pro | Trp | Val | Leu | Gly | Arg | Leu | Val | Asp | 50 | 55 | 60 | |
| Asp | Val | Ile | Ala | Asp | Ala | Pro | Val | Ser | Arg | Ile | Ala | Gly | Arg | Val | Ala | 65 | 70 | 75 | 80 |
| Val | Ile | Ala | Gly | Ala | Ala | Val | Leu | Thr | Gly | Leu | Leu | Thr | Ala | Ala | Gly | 85 | 90 | 95 | |
| Ala | Ala | Leu | Ala | Ser | Arg | Leu | Gly | Glu | Thr | Val | Leu | Ala | Arg | Leu | Arg | 100 | 105 | 110 | |
| Glu | Arg | Val | Leu | Asp | Arg | Ala | Leu | His | Leu | Pro | Ser | Ala | Thr | Leu | Glu | 115 | 120 | 125 | |
| Arg | Ala | Gly | Thr | Gly | Asp | Leu | Leu | Ala | Arg | Val | Gly | Asp | Asp | Val | Ala | 130 | 135 | 140 | |
| Val | Val | Thr | Asn | Val | Ile | Ala | Val | Ser | Gly | Pro | Ala | Phe | Val | Gly | Ala | 145 | 150 | 155 | 160 |
| Leu | Leu | Ser | Val | Val | Leu | Thr | Val | Phe | Gly | Leu | Val | Ala | Leu | Asp | Trp | 165 | 170 | 175 | |
| Arg | Leu | Gly | Leu | Ala | Gly | Leu | Val | Ala | Ala | Pro | Ala | Tyr | Ala | Leu | Ala | 180 | 185 | 190 | |
| Leu | Arg | Trp | Tyr | Leu | Arg | Arg | Ser | Ala | Pro | Tyr | Tyr | Ala | Arg | Glu | Arg | 195 | 200 | 205 | |
| Val | Ala | Thr | Gly | Glu | Arg | Thr | Gln | Ala | Met | Ala | Gly | Ala | Leu | Arg | Gly | 210 | 215 | 220 | |

Ala Ala Thr Val Arg Ala Tyr Arg Thr Glu Asp Ala His Val Ala Ala
 225 230 235 240
 Ile Ala Glu Arg Ser Gly Val Ala Arg Asp Leu Ser Leu Glu Ile Phe
 245 250 255
 Asn Leu His Thr Arg Phe Gly Leu Arg Ile Asn Arg Ser Glu Phe Leu
 260 265 270
 Gly Leu Ala Ala Val Leu Val Ala Gly Phe Phe Leu Val Arg Ala Asp
 275 280 285
 Leu Val Thr Val Gly Ala Ala Thr Thr Ala Ala Leu Tyr Phe His Arg
 290 295 300
 Leu Phe Asn Pro Ile Gly Leu Leu Leu Met Glu Ser Asp Ser Val Leu
 305 310 315 320
 Gln Ala Gly Ala Ser Leu Ala Arg Leu Val Gly Val Ala Thr Leu Pro
 325 330 335
 Asp Thr Ala Pro Ser Gly Pro Ala Pro Ser Ala Ala Gly Arg Arg Gly
 340 345 350
 Pro Ala Ala Leu Asp Val Thr Val Arg Arg His Arg Tyr Asp Asp Asp
 355 360 365
 Gly Pro Leu Val Leu Ala Asp Val Asp Leu Arg Leu Ala Pro Gly Glu
 370 375 380
 Arg Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Ser Thr Leu Ala
 385 390 395 400
 Gly Ile Ala Ala Gly Ile Ile Ala Pro Thr Asp Gly Ser Val Arg Leu
 405 410 415
 Gly Gly Val Pro Leu Thr Glu Arg Gly Glu His Ala Val Arg Arg Asp
 420 425 430
 Val Ala Leu Val Ser Gln Glu Val His Val Phe Ala Gly Pro Leu Ala
 435 440 445
 Glu Asp Leu Arg Leu Ala Ala Pro Asp Ala Thr Asp Ala Glu Leu Leu
 450 455 460
 Asp Ala Leu Asp Arg Val Gly Ala Thr Thr Trp Leu Arg Ala Leu Pro
 465 470 475 480
 Asp Gly Leu Ala Thr Ala Val Gly Glu Gly Gly His Arg Leu Thr Ala
 485 490 495
 Ala Gln Ala Gln Gln Val Ala Leu Ala Arg Leu Val Leu Ala Ala Pro
 500 505 510
 Ala Val Ala Val Leu Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly
 515 520 525

Ala Arg Asp Leu Asp Arg Ala Ala Leu Ala Ala Thr Glu Gly Arg Thr
530 535 540

Thr Leu Ile Val Ala His Arg Leu Ser Gln Ala Val Ala Ala Asp Arg
545 550 555 560

Ile Val Leu Leu Asp His Gly Arg Ile Val Glu Gln Gly Thr His Ser
565 570 575

Glu Leu Leu Ala Ala Asp Gly Arg Tyr Gly His Leu Trp Arg Ser Trp
580 585 590

Ser Val Pro Val
595

<210> 83

<211> 1791

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 83

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| cggcggacct ggacgacgct cggcgcgagg ttccgcccgc ggcccggcct cagcgccgcc | 120 |
| gcgaccgccg tgctcgctgc cgccgccacc ggccgggctgg tcgcccctg ggtgctcggc | 180 |
| cgcctcgctc acgacgtcat cgccgacgcc ccggtctccc ggatcgccgg ccgggtggcg | 240 |
| gtgatcgccg gcgcggcagt gctcaccgga ctgctcaccg ccgccggggc cgcgctcgcg | 300 |
| tcccgcttgg gggagacggt gctggcccgc ctgcgcgagc gggtcctcga ccgggagctg | 360 |
| cacctgccct cggcgacgct ggaacggggc ggacccggcg acctgctggc ccgggtcggc | 420 |
| gacgacgtgg cggtggtgac gaacgtgatc gcggtcagcg gcccggcgtt cgtcggcgcg | 480 |
| ctgctgtccg tgggtgctgac cgtgttcggg ctggtcgcgc tcgactggcg gctcggcctc | 540 |
| gccgggctgg tcgccgcgc cgctacgcg ctggcgctgc gctggtacct gcgccggtcg | 600 |
| gcgccgtact acgcccgcga gcgcgtcgcc accggcgagc ggacgcaggc gatggccggc | 660 |
| gcgctgcgtg gcgcggccac cgtgcgcgcg taccggaccg aggacgcga cgtcgcggcg | 720 |
| atcgccgagc gctccggcgt ggcgcgcgac ctgtcgctgg agatcttcaa cctgcacacc | 780 |
| cggttcgggc tgcggatcaa caggtcggag ttctcggcc tggccgggt gctcgctgcc | 840 |
| gggttcttcc tgggtccgcg cgacctggtc acagtggcg cgccgaccac cgccgcgctc | 900 |
| tacttccacc ggctgttcaa cccgatcggc ctgctgctga tggagtccga ctcgggtgctg | 960 |
| caggccggcg cgagcctcgc ccggctggtc ggcgtaggca cgctgcccga caccgccccg | 1020 |
| tccggggccc cgccgtcggc ggccggggcg cgcggcccgc cggcgctgga cgtcacggtc | 1080 |

cgccggcacc gctacgacga cgacggccct ctggtcctgg cgcacgtcga cctgcgcctg 1140
 gccccgggcg agcgggtcgc gctcgtgggc gccagcggcg cgggcaagag cacgctcgcc 1200
 ggcacgcgcg ccgggatcat cgcgccacc gacgggtcgg tacgcctggg cggcgtgccg 1260
 ctgaccgagc ggggcgagca cgccgtgcgg cgcgacgtcg cgctggtcag ccaggagggtg 1320
 cacgtcttcg ctggaccgct cgccgaggat ctgcgcctgg ctgccccgga cgccaccgac 1380
 gccgaactgc tcgacgcgct ggaccgggtc ggcgccacca cctggctgcg cgcgctgccg 1440
 gacgggctgg ccacagcggg cggcgagggc ggccaccggc tcaccgccgc gcaggcccag 1500
 caggtcgccc tggcccggct ggtgctggcc gcgccgccg tcgccgtgct ggacgaggcc 1560
 accgccgagg ccggcagcgc cggagcgcgt gacctggacc gggcggcgct ggccgccacc 1620
 gagggacgga ccacgtgat cgtggcgcac cggtcagcc aggcggtcgc cgccgaccgg 1680
 atcgtcctgc tcgaccagg gcggatcgtg gagcagggca cgcactcgga actgctcgcc 1740
 gccgacggcc ggtacgggca tctgtggcgc tcctggagcg tcccggtatg a 1791

<210> 84

<211> 507

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 84

Met Thr Asp Ala Pro Ala Arg Phe Val Leu Phe Pro Gly Arg His His
 1 5 10 15

Leu Leu Thr Arg Phe Gln Ala Asp Tyr Leu Arg Arg Leu Ala Gly Asp
 20 25 30

Asp Ala Thr Val Val Trp Ala Val Thr Ser Ala Asn His Glu Asn Thr
 35 40 45

Arg Arg Asn Pro Val Pro Tyr His Arg Arg Glu Ala Ala Ile Glu Arg
 50 55 60

Phe Ser Val Leu Ser Gly Leu Arg Ser Val Val Val Pro Ile Phe Asp
 65 70 75 80

Thr Ala Tyr Thr Asp Ala Phe Ala Glu Val Thr Leu Lys Ser Ile Ala
 85 90 95

Val Ala Thr Gly Leu Glu Leu Thr Pro Ala Asp Thr Val Leu Ala Cys
 100 105 110

Ser Thr Pro Glu Val Ala Lys Leu Tyr Glu Gln Leu Gly Phe Ser Ile
 115 120 125

Ala Pro Val Glu Ala Asp Pro Asp Leu Pro Glu Pro Pro Glu Arg Pro

| 130 | 135 | 140 |
|--|-----|-----|
| Trp Asp Val Leu Leu Arg Leu Ala Ala Gly Asp Glu Thr Trp Arg Ala 145 150 155 160 | | |
| Leu Thr His Pro Ala Thr Ile Asp Val Phe Glu Arg Tyr Arg Leu Val 165 170 175 | | |
| Glu Ser Ile Arg Ser Val Val Asn Asp Pro Leu Val Gly Asp Glu Gly 180 185 190 | | |
| Gly Leu Thr Val Thr Arg Asp Tyr Arg Thr Tyr Val Glu Ala Phe Ala 195 200 205 | | |
| Thr Ala Ala Gln Arg Lys Trp Asp Ser Val Arg Arg Tyr Val Gln Pro 210 215 220 | | |
| Gly Arg Ile Val Asp Ile Gly Cys Gly Ala Gly Ala Val Leu Glu Leu 225 230 235 240 | | |
| Ala Asp Arg Glu Ala Ala Leu Arg Glu Ser Asp Leu Ile Gly Val Glu 245 250 255 | | |
| Val Ala Arg His Leu Tyr Gln Glu Cys Leu His Lys Lys Ala Gln Gly 260 265 270 | | |
| Val Phe Arg Asn Ala Asn Val Tyr Phe Phe His Arg Asn Val Leu Gly 275 280 285 | | |
| Gly Ala Val Phe Lys Asp Arg Ser Val Asp Thr Thr Leu Thr Phe Ala 290 295 300 | | |
| Leu Thr His Glu Ile Trp Ser Tyr Gly Arg Arg Arg Glu Ser Leu Leu 305 310 315 320 | | |
| Gln Phe Ala Arg Arg Ile His Asp His Thr Val Pro Gly Gly Val Trp 325 330 335 | | |
| Ile Asn Ser Asp Val Cys Gly Pro Asp Asp Pro Arg Arg Gln Val Leu 340 345 350 | | |
| Leu Arg Leu Ser Thr Asp Asp Gly Asp Asn Pro Ala Ala Pro Arg Pro 355 360 365 | | |
| Asp Leu Ala Glu Leu Thr Ser Ala Glu Val Arg Arg Tyr Val Gly Gly 370 375 380 | | |
| Leu Ser Thr Arg Ala Arg Leu Asp Gln Phe Ala Val Asp Phe Ala Phe 385 390 395 400 | | |
| Asp Phe Asp Tyr Glu Pro Leu Pro Asp Gly Ala Val Arg Leu Thr Leu 405 410 415 | | |
| Gly Ala Ala Met Asp Tyr Leu Thr Arg Lys Asp Tyr Thr Asp Asn Trp 420 425 430 | | |
| Leu Ser Glu Thr Gln Glu Gln Phe Cys Gly Leu Ser Phe Ala Asp Trp | | |

| | | |
|---|-----|-----|
| 435 | 440 | 445 |
| Thr Asp Leu Leu Thr Glu Ala Gly Phe Glu Ile Gly Pro Ala Ser Ala | | |
| 450 | 455 | 460 |
| Pro Val Arg Asn Glu Trp Val Ile Asp Asn Arg Ile Ala Pro Val Ala | | |
| 465 | 470 | 475 |
| Ser Leu Thr Asp Leu Asp Gly Arg Pro Leu Asp Trp Pro Thr Thr His | | |
| 485 | 490 | 495 |
| Val Leu Thr Val Ala His Arg Pro Arg Asn Gln | | |
| 500 | 505 | |

<210> 85
 <211> 1524
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 85
 atgaccgacg cgccggcccg cttcgtgctc ttcccggggc ggcaccacct gctgaccgcg 60
 ttccaggccg actacctgcg gcggctggcc ggggacgacg ccacagtggc ctgggcggtg 120
 acgtcggcca accacgagaa caccaggcgc aacccggtgc cctaccaccg gcgggaggcc 180
 gcgatcgaac gattcagcgt gctgagcggg ctgcgctcgg tgggtggcgcc gatcttcgac 240
 accgcgtaca ccgacgcgtt cgccgaggtg acgctgaagt ccatcgcggt ggccaccggg 300
 ctcgaactca ccccgccga caccgtgctg gcctgctcca cgccggaggt cggaagctg 360
 tacgagcagc tcggcttttc gatcgcgccg gtcgaggcgg acccgacct gcccagaccg 420
 cccgaacggc cgtgggacgt gctgctgcgc ctggccgccc gggacgagac ctggcgcgcg 480
 ctcacccacc cggccaccat cgacgtgttc gagcgctacc gcctggtcga gtcgatccgg 540
 tcggtggtga acgaccgct cgtcggcgac gaggcggtc tcacagtac ccgcgactac 600
 cggacctacg tcgaggcgtt cgccacggcc gcgcagcgca agtgggactc ggtacgccgg 660
 tacgtgcagc ccggccgcat cgtggacatc ggctgcggcg cgggcgccgt cctggaactc 720
 gccgaccggg aggccgcgct gcgtgagagc gacctgatcg gcgtggaggt cgcccgccac 780
 ctctaccagg agtgctgca caagaaggcg caggcggtgt tccgcaacgc caacgtctac 840
 ttcttccacc gcaacgtcct cgggcgcgcg gtgttcaagg accgctcggt cgacaccacg 900
 ctcacgttcg cgctgaccca cgagatctgg tcgtacgggc ggcgcgggga gtcgctgctg 960
 cagttcgccc gccgcatcca cgaccacacg gtgcccggcg gcgtctggat caacagcgac 1020
 gtgtgcggtc cggacgaccc ccggcggcag gtgctcctgc gactgtccac cgacgacggc 1080
 gacaacccgg ccgcgccccg ccccgacctc gccgagctga cctcggcgga ggtccggcgt 1140

tacgtcggcg ggctgtcgac gcgggcgcgg ctggaccagt tcgccgtcga cttcgcgttc 1200
gacttcgact acgagccgct ccccgacggc gcggtacgcc tgacgctggg cgccgcgatg 1260
gactacctga cccgcaagga ctacacggac aactggctgt cggagacgca ggagcagttc 1320
tgccggcctga gcttcgccga ctggacggac ctgctcaccg aggcgggggtt cgagatcggc 1380
ccggcgctcg cgccggtgcg caacgagtgg gtgatcgaca accggatcgc gccagtcgcy 1440
tcctcaccg acctcgacgg ccggccgctg gactggccga ccaccacgt cctcaccgtc 1500
gccaccgcc cccgcaacca gtga 1524

<210> 86

<211> 232

<212> PRT

<213> Micromonospora sp. strain 046-EC011

<400> 86

Val Ser Asp Ile Gln Ile Ile Ser Phe Val Ala Ala Ser Leu Leu Ile
1 5 10 15

Ile Ile Val Pro Gly Val Asp Phe Ala Leu Val Thr Arg Gln Thr Val
20 25 30

Arg Tyr Gly Arg Arg Ala Gly Phe Val Val Leu Ala Gly Leu Phe Val
35 40 45

Ala Ala Leu Val His Ala Ser Phe Ala Thr Ala Gly Leu Ser Ala Leu
50 55 60

Leu Val Ser Ser Pro Thr Leu Tyr Thr Val Leu Arg Val Ala Gly Ala
65 70 75 80

Leu Tyr Leu Leu Tyr Leu Gly Gly Thr Ile Leu Trp Ala Thr Arg Pro
85 90 95

Arg Arg Thr Val Pro Ala Ala Gln Pro Val Thr Val Gly Ala Gly Gly
100 105 110

Ala Gly Pro Asp Thr Asp Thr Gly Pro Ala Pro Val Pro Asp Thr Pro
115 120 125

Ala Ala Asp Glu Pro His Val Ala Arg Arg Ser Phe Val Met Gly Val
130 135 140

Thr Ser Gln Leu Leu Asn Val Lys Val Val Val Phe Tyr Val Ser Phe
145 150 155 160

Val Pro Gln Phe Val Lys Pro Gly Glu Gly Ala Ala Ala Arg Thr Ala
165 170 175

Val Leu Ala Ala Thr Phe Ile Gly Leu Ala Val Leu Trp Trp Ala Cys

180 185 190
 Tyr Ile Met Leu Ile Asp Arg Leu Gln Pro Trp Leu Thr Arg Pro Ser
 195 200 205
 Val Leu Leu Val Ile Glu Arg Leu Thr Gly Leu Ile Leu Ile Val Leu
 210 215 220
 Ala Ile Arg Ile Ala Leu Ser Arg
 225 230

<210> 87
 <211> 699
 <212> DNA
 <213> Micromonospora sp. strain 046-EC011

<400> 87
 gtgtctgaca tccagatcat cagtttcgtc gccgccagcc tgetcatcat catcgtgccg 60
 ggcgtcgact tcgcgctcgt caccggcgag accgtcaggt acggccggcg ggccgggttc 120
 gtggtgctgg cggggtgtt cgtcgccgcg ctggtgcacg cgtcgttcgc gaccgccggc 180
 ctgtccgccc tgctggtctc ctcgccgacg ctctacacgg tgctgcgcgt cgccggcgcg 240
 ctgtacctgc tctacctggg cggcacgacg ctctgggcca cccggccgcg ccggacggtc 300
 ccggcggcgc agccggtcac tgtcggcgcg ggccggcgcc ggccggacac ggacaccggc 360
 cccgcgcggg tgccggacac cccggccgcc gacgagccgc acgtggcccg ccgctcgttc 420
 gtcattggcg tcaccagcca gctgctgaac gtcaaggtgg tcgtcttcta cgtctcgttc 480
 gtgccgcagt tcgtcaagcc cggcgagggg gcgccggccc gtacggcggt gtcgcccgcc 540
 acgttcacgc gcctcgcggt gctctggtgg gcctgtaca tcatgtcat cgacagggtg 600
 cagccctggc tgaccgggcc gtccgtgctg ctggtgatcg aacggctgac cgggctcatc 660
 ctgatcgtcc tggcgatccg gatcgcgctg agccggtga 699

<210> 88
 <211> 132
 <212> PRT
 <213> Micromonospora sp. strain 046-EC011

<400> 88

Val Gly Val Ser Ala Met Thr Thr Phe Asp Tyr Asp Gly Arg Val Phe
 1 5 10 15

Val Ser Val Asp His Asp Ala Gly Asp Gly Ala Glu Pro Leu Arg Gly
 20 25 30

His Tyr His Gln Arg Gly Asp Leu Val Trp Ala Glu Ile Thr Gly Gly
 35 40 45

Pro Val Arg His Gly Arg Leu Ala Gly Thr Cys Asp Ala Gln Gly Val
50 55 60

Val Arg Phe Ala Tyr Leu Glu Val Leu Thr Asp Gly Thr Ile Val Ile
65 70 75 80

Gly Glu Cys Glu Ser Arg Pro Glu Arg Leu Pro Asp Gly Arg Ile Arg
85 90 95

Leu Arg Glu Gln Trp Arg Arg His Gly Pro Arg Gln Asp Ser Gly Val
100 105 110

Ser Val Ile Glu Glu Ala Val Pro Ala Leu Ala Gly Gly Gln Glu Ser
115 120 125

Arg Arg Arg Val
130

<210> 89

<211> 399

<212> DNA

<213> Micromonospora sp. strain 046-EC011

<400> 89

gtgggctga gcgcgatgac gacattcgac tacgacggcc gcgtcttcgt ctcggtggac 60

cacgacgcc gtgacggcgc cgagccgctg cgggggcaact accaccagcg tggcgacctg 120

gtctgggcgg agatcaccgg cggcccggtc cggcacggcc ggctggccgg cacctgcgac 180

gcgcagggcg tcgtgcgctt cgcctacctg gaggtgctca ccgacggcac catagtcac 240

ggcgagtgcg agtcccggcc cgaacggctg ccggacggcc ggatccggct gcgggaacag 300

tggcgccggc acggaccacg ccaggacagc ggcgtctccg tcatcgagga ggcagtgcg 360

gcgctcgccg gaggacagga gagccggcgt cgtgtctga 399